

REFERENCE/DOCKET NUMBER: 28111/34800
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-767-395-6

Query Match 89.7%; Score 26; DB 10; Length 32;
Best Local Similarity 80.0%; Pred. No. 19;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTMH 5
|||:
9 SYTLL 13

RESULT 2

US-083-357-712
; since 712, Application US/10083357
; Publication No. US20030054370A1
; GENERAL INFORMATION:
; APPLICANT: Qiantong Zeng et al.
; TITLE OF INVENTION: Systemic Discovery of New Genes
; FILE REFERENCE: 032796-090
; CURRENT APPLICATION NUMBER: US/10/083,357
; CURRENT FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 1346
; SEQ ID NO 712
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-083-357-712

Query Match 89.7%; Score 26; DB 9; Length 82;
Best Local Similarity 80.0%; Pred. No. 47;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTMH 5
|||:
Db 1 NYTMH 5

RESULT 3
US-09-903-456-20
; Sequence 20, Application US/09903456
; Patent No. US20020138874A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407 US P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-903-456-20

Query Match 89.7%; Score 26; DB 10; Length 238;

Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYTMH 5
|||:
Db 232 SYTLL 236

RESULT 4

US-10-043-487-407
; Sequence 407, Application US/10043487
; Publication No. US20030055220A1
; GENERAL INFORMATION:
; APPLICANT: HYBRIGENICS
; APPLICANT: PIERRE, LEGRAIN
; TITLE OF INVENTION: Protein-protein interactions between Shigella flexneri polypeptide
; FILE REFERENCE: B4778A
; CURRENT APPLICATION NUMBER: US/10/043,487
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/261,130
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 561
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 407
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Shigella flexneri
US-10-043-487-407

Query Match 89.7%; Score 26; DB 9; Length 335;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTMH 5
|||:
Db 119 SYTLL 123

RESULT 5
US-09-925-301-984
; Sequence 984, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 984
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-984

Query Match 89.7%; Score 26; DB 10; Length 402;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTMH 5
|||:
Db 116 SYTLL 120

RESULT 6

US-09-742-580-8
; Sequence 8, Application US/09742580

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 17:21:54 ; Search time 1.47368 Seconds
(without alignments)
256.547 Million cell updates/sec

Title: US-09-644-668a-27

Perfect score: 29

Sequence: 1 SYTMH 5

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 288829 seqs, 75613885 residues

Total number of hits satisfying chosen parameters: 288829

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB pep.*
7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	26	89.7	32 10 US-09-767-395-8	Sequence 8, Appl1
2	26	89.7	82 9 US-10-083-357-712	Sequence 712, Appl
3	26	89.7	238 10 US-09-903-456-20	Sequence 407, Appl
4	26	89.7	335 9 US-10-043-487-407	Sequence 2, Appl1
5	26	89.7	402 10 US-09-925-301-984	Sequence 984, Appl
6	26	89.7	505 9 US-09-742-580-8	Sequence 8, Appl1
7	26	89.7	505 10 US-09-742-581-8	Sequence 8, Appl1
8	26	89.7	505 10 US-09-742-582-8	Sequence 8, Appl1
9	26	89.7	836 10 US-09-953-688a-7	Sequence 7, Appl1
10	26	89.7	86 10 US-09-864-761-39492	Sequence 39492, A
11	25	86.2	99 9 US-10-194-975-27	Sequence 27, Appl
12	25	86.2	117 9 US-09-956-206A-76	Sequence 76, Appl
13	25	86.2	117 9 US-09-956-206A-78	Sequence 78, Appl
14	25	86.2	119 9 US-09-813-398-2	Sequence 2, Appl1
15	25	86.2	119 9 US-09-795-515-11	Sequence 11, Appl
16	25	86.2	119 9 US-09-795-515-12	Sequence 12, Appl
17	25	86.2	119 9 US-09-795-515-13	Sequence 13, Appl
18	25	86.2	119 9 US-09-795-515-14	Sequence 14, Appl
19	25	86.2	119 9 US-09-795-515-15	Sequence 15, Appl

20	25	86.2	119 9 US-09-795-515-16	Sequence 16, Appl
21	25	86.2	119 9 US-09-795-515-17	Sequence 17, Appl
22	25	86.2	119 9 US-09-795-515-18	Sequence 18, Appl
23	25	86.2	119 9 US-09-795-515-19	Sequence 19, Appl
24	25	86.2	119 9 US-09-795-515-20	Sequence 20, Appl
25	25	86.2	119 9 US-09-795-515-21	Sequence 21, Appl
26	25	86.2	119 9 US-09-795-515-22	Sequence 22, Appl
27	25	86.2	119 9 US-09-795-515-23	Sequence 23, Appl
28	25	86.2	119 9 US-09-795-515-24	Sequence 24, Appl
29	25	86.2	119 9 US-09-795-515-30	Sequence 30, Appl
30	25	86.2	127 9 US-09-848-798-27	Sequence 27, Appl
31	25	86.2	131 9 US-09-848-798-28	Sequence 28, Appl
32	25	86.2	136 9 US-09-956-206A-47	Sequence 47, Appl
33	25	86.2	136 9 US-09-956-206A-63	Sequence 63, Appl
34	25	86.2	138 12 US-10-066-895-6	Sequence 6, Appl1
35	25	86.2	138 12 US-10-066-895-7	Sequence 7, Appl1
36	25	86.2	138 12 US-10-066-895-8	Sequence 8, Appl1
37	25	86.2	139 12 US-10-066-895-5	Sequence 5, Appl1
38	25	86.2	169 10 US-09-867-550-682	Sequence 682, Appl
39	25	86.2	209 10 US-09-393-634-13	Sequence 13, Appl
40	25	86.2	232 10 US-09-754-998-2	Sequence 2, Appl1
41	25	86.2	232 10 US-09-864-761-33560	Sequence 33560, A
42	25	86.2	232 10 US-09-864-761-34077	Sequence 34077, A
43	25	86.2	232 10 US-09-811-384-10	Sequence 10, Appl
44	25	86.2	241 10 US-09-940-166A-1	Sequence 1, Appl
45	25	86.2	247 9 US-09-880-748-1307	Sequence 1307, Appl

ALIGNMENTS

RESULT 1
US-09-767-395-8
Sequence 8, Application US/09767395
Patent No. US2002004215A1
GENERAL INFORMATION:
APPLICANT: Osbourn, Jane K
Derbyshire, Elaine J
McCafferty, John G
Vaughan, Tristan J
Johnson, Kevin S
TITLE OF INVENTION: Labelling and selection of molecules
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09767395
FILING DATE: 23-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/098,244
FILING DATE: <Unknown>
APPLICATION NUMBER: PCT/GB97/01835
FILING DATE: 08-JUL-1997
APPLICATION NUMBER: GB 9624293.2
FILING DATE: 08-JUL-1996
APPLICATION NUMBER: GB 9624880.2
FILING DATE: 29-NOV-1996
APPLICATION NUMBER: GB 9712816.5
FILING DATE: 18-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107

RT divergence in early regulation and replication regions.",
 RL DNA Res. 6:235-240(1999).
 (5)
 RP SEQUENCE FROM N.A.
 RC SPECIES-STX converting bacteriophage I; STRAIN-STX2 PHAGE-I;
 RA Sato T., Shimizu T., Watarai M., Kobayashi M., Kano S., Hamabata T.,
 Yamazaki S., Takeda Y.;
 RT "Genomic sequence of Shiga toxin 2-converting phage isolated from
 Escherichia coli O157:H7 Okayama strain and comparison with other
 Shiga toxin 2-converting phages";
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF125520; AAD25413.1; -
 DR EMBL: AP000363; BA84290.1; -
 DR EMBL: AP004402; BA87939.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 95 AA; 10446 MW; 5F2FB7C449685BAC CRC64;
 Query Match 100.0%; Score 29; DB 9; Length 95;
 Best Local Similarity 100.0%; Pred. No. 9.6;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYTMH 5
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 DB 30 SYTMH 34
 RESULT 2
 09KXG9 PRELIMINARY; PRT; 95 AA.
 AC 09KXG9;
 DT 01-OCT-2000 (TEMBLrel. 15, Created)
 DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
 DE Hypothetical protein H0078.
 GN H0078 OR EC31157.
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=83334;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7;
 MEDLINE=20198780; PubMed=10734605;
 RA Makino K., Yokoyama K., Kubota Y., Yutsudo C.H., Kimura S.,
 Kurokawa K., Ishii K., Hattori M., Tetsuno I., Abe H., Iida T.,
 Yamamoto K., Ohnishi M., Hayashi T., Yasunaga T., Honda T.,
 Sasaki C., Shingawa H.;
 RT "Complete nucleotide sequence of the prophage VT2-Sakai carrying the
 verotoxin 2 genes of the enterohemorrhagic Escherichia coli O157:H7
 derived from the Sakai outbreak";
 RL Genes Genet. Syst. 74:227-239(1999).
 (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / RIMD 0509952;
 MEDLINE=21156231; PubMed=11258796;
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,
 Kihara S., Shiba T., Hattori M., Shingawa H.;
 RT "Complete genome sequence of enterohemorrhagic Escherichia coli
 O157:H7 and genomic comparison with a laboratory strain K-12";
 RL DNA Res. 8:11-22(2001).
 DR EMBL: AF000422; BA94106.1; -
 DR EMBL: AP002554; BA834590.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 95 AA; 10446 MW; 5F2FB7C449685BAC CRC64;
 Query Match 100.0%; Score 29; DB 16; Length 95;
 Best Local Similarity 100.0%; Pred. No. 9.6;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYTMH 5
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DB 30 SYTMH 34
 RESULT 3
 09STC7 PRELIMINARY; PRT; 123 AA.
 AC 09STC7;
 DT 01-DEC-2001 (TEMBLrel. 19, Created)
 DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
 DE GH01923p.
 GN CG6783.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RA Stapleton M., Brokstein P., Hong L., Agdayant A., Carlson J.,
 Champe M., Chavez C., Dorsett V., Fattan D., Frise B., George R.,
 Gonzalez M., Guatin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nuno J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celisner S.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY060229; AAL25268.1; -
 DR FLYBASE; FBgn0037913; CG6783.
 SQ SEQUENCE 123 AA; 14109 MW; 838C453CEB4CEB7F CRC64;
 Query Match 100.0%; Score 29; DB 5; Length 123;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYTMH 5
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 DB 95 SYTMH 99
 RESULT 4
 096687 PRELIMINARY; PRT; 242 AA.
 AC 096687;
 DT 01-MAY-1999 (TEMBLrel. 10, Created)
 DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
 DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
 DE Fibrinolytic enzyme (Fragment).
 OS Lumbricus bimaculatus.
 OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplochaeta;
 OC Lumbricina; Lumbricidae; Lumbricus.
 OX NCBI_TaxID=86417;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Liang G., Meng X., Fu S., Li L., Hou Y., Chen F., Qian Y.;
 RT "Cloning of the genes encoding fibrinolytic enzymes from Lumbricus
 bimaculatus";
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 CC EMBL: AF109648; AAD05563.1; -
 DR HSSP; P20231; IAAO.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR001254; Ser-protease_Try.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; TRYP SPc; 1.
 DR PROSITE; PS00240; TRYP SIN DOM; 1.
 DR PROSITE; PS00134; TRYP SIN HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYP SIN SER; 1.
 KW Hydrolyase; Serine protease.
 FT NON TER 1
 SQ SEQUENCE 242 AA; 24837 MW; F912425D2724745D CRC64;

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using SW model

Run on: April 16, 2003, 17:13:59 / Search time 5.12281 seconds
(without alignments)

201.108 Million cell updates/sec

Title: US-09-644-668a-27

Perfect score: 29

Sequence: 1 SYTM 5

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

TC number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_prodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeophages:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	95	9 O9XJH3	O9XJH3 bacteriophage
2	29	100.0	95	16 O9XJG9	O9XJG9 escherichia
3	29	100.0	123	5 O9STC7	O9STC7 drosophila
4	29	100.0	242	5 O96687	O96687 lumbricus b
5	29	100.0	388	17 O8T130	O8T130 methanobac
6	29	100.0	945	5 O93378	O93378 caenorhabd
7	29	89.7	56	2 O52223	O52223 leucostoc
8	29	89.7	94	17 O9HRT2	O9HRT2 thermophil
9	29	89.7	113	2 O93189	O93189 staphylococ
10	29	89.7	121	4 O9UM10	O9UM10 homo sapien
11	29	89.7	132	4 O9UC94	O9UC94 homo sapien
12	29	89.7	143	4 O9UNR4	O9UNR4 homo sapien
13	29	89.7	143	4 O16502	O16502 homo sapien
14	29	89.7	144	4 O13830	O13830 homo sapien
15	29	89.7	157	1 P94805	P94805 haloterrax s
16	29	89.7	158	4 O15229	O15229 homo sapien

17	26	89.7	171	10 O9ATP4	O9ATP4 pennisetum
18	26	89.7	178	10 O9XFI7	O9XFI7 rosa hybrid
19	26	89.7	178	17 O9UPP4	O9UPP4 pyrococcus
20	26	89.7	190	8 O9B3V2	O9B3V2 plethodon g
21	26	89.7	190	8 O9B3U4	O9B3U4 plethodon p
22	26	89.7	192	8 O9B3U8	O9B3U8 plethodon t
23	26	89.7	200	8 O9B3U3	O9B3U3 plethodon y
24	26	89.7	203	8 O9B3V3	O9B3V3 plethodon f
25	26	89.7	213	16 O9XZD7	O9XZD7 raietonia s
26	26	89.7	216	12 O69574	O69574 human herpe
27	26	89.7	218	8 O9B3U2	O9B3U2 plethodon w
28	26	89.7	220	8 O9B3U9	O9B3U9 plethodon o
29	26	89.7	231	8 O79474	O79474 pelamis pla
30	26	89.7	231	8 O8WA07	O8WA07 demansia at
31	26	89.7	231	8 O8WA04	O8WA04 homocorrelap
32	26	89.7	231	8 O8WA03	O8WA03 latiscada c
33	26	89.7	231	8 O8WA00	O8WA00 notechis at
34	26	89.7	236	4 O9UEA4	O9UEA4 homo sapien
35	26	89.7	248	16 O9X866	O9X866 streptomyce
36	26	89.7	281	5 O20904	O20904 caenorhabd
37	26	89.7	306	11 O99XR1	O99XR1 mus musculu
38	26	89.7	318	16 O51270	O51270 borrelia bu
39	26	89.7	319	16 O8XV04	O8XV04 raietonia s
40	26	89.7	324	4 O9UPK9	O9UPK9 homo sapien
41	26	89.7	326	4 O9UPK8	O9UPK8 homo sapien
42	26	89.7	326	4 O13048	O13048 homo sapien
43	26	89.7	332	4 O15242	O15242 homo sapien
44	26	89.7	333	4 O75238	O75238 homo sapien
45	26	89.7	335	4 O15239	O15239 homo sapien

ALIGNMENTS

RESULT 1
O9XJH3 PRELIMINARY; PRT; 95 AA.
ID O9XJH3
AC O9XJH3
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Hypothetical 10.4 kDa protein.
GN L0068.
OS Bacteriophage 933W,
OS Bacteriophage VT2-Sa, and
OS Stx2 converting bacteriophage I.
OC Viruses; dsDNA viruses, no RNA stage; unclassified dsDNA phages.
OX NCBI_TaxID=10730, 97081, 180816;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Phage 933W;
RA MEDLINE=99173898; PubMed=10074068;
RX Plunkett G. III, Rose D.J., Durfee T.J., Blattner F.R.,
RT "Sequence of Shiga toxin 2 phage 933W from Escherichia coli O157:H7;
RL Shiga toxin as a phage late-gene product";
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Phage 933W;
RA Plunkett G. III;
RT J. Bacteriol. 181:1767-1778 (1999).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=Phage VT2-Sa;
RA Miyamoto H.;
RT Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=Phage VT2-Sa;
RX MEDLINE=99419919; PubMed=10492170;
RA Miyamoto H., Nakai W., Yajima N., Fujibayashi A., Higuchi T., Sato K.,
RT Matsushiro A.;
RT "Sequence analysis of Stx2-Converting phage VT2-Sa shows a great

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CC NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Frangmyr L., Teglund S., Israelsson A., Hammarstrom S.;
 RT "Characterization of upstream promoter region, exon 1 and exon 2 of the
 RL PSG gene family.";
 Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
 CC -1- DEVELOPMENTAL STAGE: PSBG ARE PRODUCED IN HIGH QUANTITY DURING
 CC PREGNANCY.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CEA
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF106552; AAD21024.1;
 DR EMBL; AF106551; AAD21024.1; JOINED.
 DR MIM; 176401;
 KW Immunoglobulin domain; Glycoprotein; Signal; Multigene family.
 FT CHAIN 1 34 POTENTIAL.
 FT SIGNAL 35 >143 PREGNANCY-SPECIFIC BETA-1-GLYCOPROTEIN
 FT DOMAIN 35 >143 IG-LIKE V-TYPE DOMAIN.
 FT SITE 127 129 CELL ATTACHMENT SITE (POTENTIAL).
 FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT NON TER 143 143
 SQ SEQUENCE 143 AA; 16065 MW; 2C452383C831D28 CRC64;
 QY Query Match 89.7%; Score 26; DB 1; Length 143;
 Best Local Similarity 80.0%; Pred. No. 19;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYTMH 5
 Db 119 SYTMH 123
 RESULT 3
 PSGH HUMAN STANDARD; PRT; 144 AA.
 ID PSGH HUMAN
 AC Q9UQ74;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Pregnancy-specific beta-1-glycoprotein 8 precursor (PSBG-8)
 DE (Fragment).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CC NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Frangmyr L., Teglund S., Israelsson A., Hammarstrom S.;
 RT "Characterization of upstream promoter region, exon 1 and exon 2 of the
 RL PSG gene family.";
 Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
 CC -1- DEVELOPMENTAL STAGE: PSBG ARE PRODUCED IN HIGH QUANTITY DURING
 CC PREGNANCY.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CEA

CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF106556; AAD21022.1;
 DR EMBL; AF106555; AAD21022.1; JOINED.
 DR Genew; HGNC.9525; PSBG.
 DR MIM; 176397;
 KW Immunoglobulin domain; Glycoprotein; Signal; Repeat; Multigene family.
 FT CHAIN 1 34 POTENTIAL.
 FT SIGNAL 35 >144 PREGNANCY-SPECIFIC BETA-1-GLYCOPROTEIN 8.
 FT DOMAIN 35 144 IG-LIKE V-TYPE DOMAIN.
 FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT NON TER 144 144
 SQ SEQUENCE 144 AA; 16109 MW; 0A83A6711042C1FE CRC64;
 QY Query Match 89.7%; Score 26; DB 1; Length 144;
 Best Local Similarity 80.0%; Pred. No. 19;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYTMH 5
 Db 119 SYTMH 123
 RESULT 4
 SCL OCTVU STANDARD; PRT; 214 AA.
 ID SCL OCTVU
 AC P27013;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE S-crystallin 1.
 GN OCTS1.
 OS Octopus vulgaris (Octopus).
 CC Eukaryota; Metazoa; Mollusca; Cephalopoda; Colecoidea; Octopoda;
 CC Incirrata; Octopodidae; Octopus.
 CC NCBI_TaxId=6645;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lens; PubMed=1627174;
 RX MEDLINE=92328840;
 RA Iln C.-W., Chlou S.-H.;
 RT "Facile cloning and sequencing of S-crystallin genes from octopus
 RT lenses based on polymerase chain reaction.";
 RL Biochem. Int. 27:173-178(1992).
 CC -1- FUNCTION: S-CRYSTALLINS ARE STRUCTURAL COMPONENTS OF SQUIDS AND
 CC OCTOPI EYE LENS. CONTAINS RELATIVELY LITTLE GST ACTIVITY (1/1000
 CC OF THAT OF MAMMALIAN GST ENZYME).
 CC -1- TISSUE SPECIFICITY: LENS.
 CC -1- SIMILARITY: BELONGS TO THE GST SUPERFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X65543; CAA46511.1;
 DR PIR; S21340; S21340.
 DR HSP; P46088; ZGSO.

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:57:42 ; Search time 0.982456 seconds
(without alignments)

211.085 Million cell updates/sec

Title: US-09-644-668a-27

Perfect score: 29

Sequence: 1 SYTMH 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	89.7	102	1 YH88_YEAST	Q04838 saccharomyc
2	26	89.7	143	1 PS6D_HUMAN	Q9UG72 homo sapien
3	26	89.7	144	1 PS68_HUMAN	Q9UG74 homo sapien
4	26	89.7	214	1 SC1_OCTVU	P27013 octopus vul
5	26	89.7	215	1 SC2_OCTVU	P27014 octopus vul
6	26	89.7	215	1 SC3_OCTVU	P27011 octopus dof
7	26	89.7	215	1 SC3_OCTVU	Q25626 octopus dof
8	26	89.7	215	1 SC4_OCTVU	P27012 octopus dof
9	26	89.7	282	1 LPXC_CHLUP	Q94792 chlamydia p
10	26	89.7	286	1 LPXC_CHLUP	Q94793 chlamydia p
11	26	89.7	286	1 LPXC_CHLUP	O84538 chlamydia t
12	26	89.7	315	1 ISPE_SYNT3	P72663 synchocyst
13	26	89.7	323	1 ARG1_SCHPO	P37818 schizosach
14	26	89.7	323	1 ARG1_SCHPO	Q10066 schizosach
15	26	89.7	335	1 ARG2_SCHPO	P11465 homo sapien
16	26	89.7	335	1 PS62_HUMAN	Q15238 homo sapien
17	26	89.7	389	1 PRS8_HUMAN	P34124 dictyostell
18	26	89.7	402	1 PRS8_HUMAN	P34814 manduca sex
19	26	89.7	402	1 PRS8_HUMAN	O18413 drosophila
20	26	89.7	405	1 PRS8_HUMAN	P47210 homo sapien
21	26	89.7	406	1 PRS8_HUMAN	P11464 homo sapien
22	26	89.7	419	1 PS61_HUMAN	Q00888 homo sapien
23	26	89.7	419	1 PS64_HUMAN	Q13046 homo sapien
24	26	89.7	424	1 PS67_HUMAN	O15235 homo sapien
25	26	89.7	424	1 PS6C_HUMAN	O75244 homo sapien
26	26	89.7	424	1 PS6G_HUMAN	O16557 homo sapien
27	26	89.7	424	1 PS6G_HUMAN	O00889 homo sapien
28	26	89.7	435	1 PS66_HUMAN	O00889 homo sapien
29	26	89.7	461	1 PRS8_HUMAN	P54871 xenopus lae
30	26	89.7	462	1 HMCS_CARBL	P64871 xenopus lae
31	26	89.7	736	1 ETR2_LYSES	O49187 lycoperisico
32	26	89.7	740	1 ETR1_CUCUR	O82436 cucumis mel
33	26	89.7	740	1 ETR1_CUCUR	O82436 cucumis sat
34	26	89.7	1748	1 POLR_ELV	P35928 erythrum la

34	26	89.7	3063	1 CA1C_HUMAN	Q09715 homo sapien
35	26	89.7	3119	1 CA1C_MOUSE	Q60847 mus musculu
36	26	89.7	3124	1 CA1C_CHICK	P13944 gallus gall
37	25	86.2	138	1 TSHB_CANFA	P54828 canis famli
38	25	86.2	138	1 TSHB_HUMAN	P01222 homo sapien
39	25	86.2	185	1 YALS_ECOLI	P71311 escherichia
40	25	86.2	219	1 HIS8_MYCSE	P28735 mycobacteri
41	25	86.2	272	1 YEGX_ECOLI	P76421 escherichia
42	25	86.2	296	1 ARG1_BACSU	P39138 bacillus su
43	25	86.2	297	1 Y060_MYCSE	P47306 mycoplasma
44	25	86.2	299	1 ARG1_BACCD	P53608 bacillus ca
45	25	86.2	309	1 YERY_ECOLI	P76369 escherichia

ALIGNMENTS

RESULT 1

YH88_YEAST STANDARD; PRT; 102 AA.

AC Q04838;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Very hypothetical 11.8 kDa protein in HOR7-COX7 intergenic region.
GN YH8254C OR YH9920.08C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RA Hunt S., Bowman S., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@ebi.ac.uk).CC
CC EMBL; Z4639; CA88581.1; -
DR SGD; S0004867; YMR254C.
KW Hypothetical protein; Transmembrane.
DR TRANSMEM 1 21
FT TRANSMEM 42 62 POTENTIAL.
FT TRANSMEM 68 88 POTENTIAL.
SQ SEQUENCE 102 AA; 11816 MW; 7AF02826F3964D CRC64;

Query Match Best Local Similarity 89.7%; Score 26; DB 1; Length 102;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYTMH 5
Db 47 TYTMH 51

RESULT 2

PS6D_HUMAN STANDARD; PRT; 143 AA.
AC Q9UG72;
DT 30-MAY-2000 (Rel. 39, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pregnancy-specific beta-1-glycoprotein 13 precursor (PSBG-13)
GN (Fragment).
DR PS613.
OS Homo sapiens (Human).

A:Pathway: detoxification
A:Note: this protein has weak catalytic activity
C:Superfamily: glutathione transferase
C:Keywords: detoxification; glutathione; transferase

Query Match 89.7%; Score 26; DB 2; Length 214;
Best Local Similarity 80.0%; Pred. No. 89;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTMH 5
|||:
Db 3 SYTLH 7

RESULT 13

S-crystallin isoform S3 - common octopus
C/Species: Octopus vulgaris (common octopus)
C/Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 18-Jun-1999
C/Accession: S56762; S37148
R: Ju. S.H.; Yu. C.W.; Lin. C.W.; Pan. F.M.; Lu. S.F.; Lee. H.J.; Chang. G.G.
Biochem. J. 309, 793-800, 1995
A/Title: Octopus S-crystallins with endogenous glutathione S-transferase (GST) activity:
A/Reference number: S56760; MUID:9536954; PMID:7639695
A/Accession: S56762
A/Molecule type: mRNA
A/Residues: 1-215 <CHI>
A/Cross-references: EMBL:X74858; NID:g400475; PIDN:CAA52850.1; PID:g400476
C:Superfamily: glutathione transferase

Query Match 89.7%; Score 26; DB 2; Length 215;
Best Local Similarity 80.0%; Pred. No. 89;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTMH 5
|||:
Db 3 SYTLH 7

RESULT 14

D41681
S-crystallin 4 - giant octopus
C/Species: Octopus doeleini (giant octopus)
C/Date: 30-Jun-1992 #sequence_revision 18-Sep-1992 #text_change 18-Jun-1999
C/Accession: D41681
R/Tomarev, S.I.; Zinovleva, R.D.; Platigorsky, J.
J. Biol. Chem. 266, 24226-24231, 1991
A/Title: Crystallins of the octopus lens. Recruitment from detoxification enzymes.
A/Reference number: A41681; MUID:92084735; PMID:1721068
A/Accession: D41681
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-215 <TOM>
A/Cross-references: GB:M65187; NID:g159734; PIDN:AAA29389.1; PID:g159735
C:Superfamily: glutathione transferase

Query Match 89.7%; Score 26; DB 2; Length 215;
Best Local Similarity 80.0%; Pred. No. 89;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTMH 5
|||:
Db 3 SYTLH 7

RESULT 15

C41681
S-crystallin 3 - giant octopus
C/Species: Octopus doeleini (giant octopus)
C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 18-Jun-1999
C/Accession: C41681
R/Tomarev, S.I.; Zinovleva, R.D.; Platigorsky, J.
J. Biol. Chem. 266, 24226-24231, 1991

A/Title: Crystallins of the octopus lens. Recruitment from detoxification enzymes.

A/Reference number: A41681; MUID:92084735; PMID:1721068

A/Accession: C41681

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-215 <TOM>

A/Cross-references: GB:M65186; NID:g159732; PIDN:AAA29388.1; PID:g159733

C:Superfamily: glutathione transferase

Query Match 89.7%; Score 26; DB 2; Length 215;
Best Local Similarity 80.0%; Pred. No. 89;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTMH 5
|||:
Db 3 SYTLH 7

Search completed: April 16, 2003, 17:21:37
Job time : 2.54386 secs

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OM protein - protein search, using sw model

Run on: April 16, 2003, 17:11:36 ; Search time 1.54386 Seconds

(without alignments)
311.344 Million cell updates/sec

Title: US-09-644-668A-27

Perfect score: 29

Sequence: 1 SYTMH 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

PIR 73:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	29	100.0	95 2 G90774	hypothetical prote
2	29	100.0	96 2 S17230	Ig heavy chain V r
3	29	100.0	96 2 S17621	Ig heavy chain V r
4	29	100.0	96 2 S17620	Ig heavy chain V r
5	29	100.0	102 2 S26471	Ig heavy chain V r
6	29	100.0	945 2 T19943	hypothetical prote
7	26	89.7	102 2 S53076	probable membrane
8	26	89.7	113 2 E33936	Ig heavy chain V r
9	26	89.7	121 2 D32268	carcinoembryonic a
10	26	89.7	157 2 T44794	hypothetical prote
11	26	89.7	178 2 C75059	hypothetical prote
12	26	89.7	214 2 S56758	S-crystallin isofo
13	26	89.7	215 2 S56762	S-crystallin isofo
14	26	89.7	215 2 D41681	S-crystallin 4 - g
15	26	89.7	215 2 C41681	S-crystallin 3 - g
16	26	89.7	215 2 S56759	S-crystallin isofo
17	26	89.7	248 2 T36093	probable DNA methy
18	26	89.7	281 2 T23791	hypothetical prote
19	26	89.7	282 2 A66572	myristoyl GlcNac d
20	26	89.7	282 2 E77051	UDP-3-O-(3-hydroxy
21	26	89.7	283 2 S52928	UDP-3-O-(3-hydroxy
22	26	89.7	286 2 D71502	UDP-3-O-(3-hydroxy
23	26	89.7	287 2 C81615	UDP-3-O-(3-hydroxy
24	26	89.7	291 2 A81662	UDP-3-O-(3-hydroxy
25	26	89.7	315 2 S74513	hypothetical prote
26	26	89.7	318 2 G70131	hypothetical prote
27	26	89.7	321 2 T52537	arginase (EC 3.5.3
28	26	89.7	323 1 S45455	arginase (EC 3.5.3
29	26	89.7	323 2 T38739	arginase - fission

30	26	89.7	324 2 G43354	pregnancy-specific
31	26	89.7	326 2 F43354	pregnancy-specific
32	26	89.7	326 2 JC4124	pregnancy-specific
33	26	89.7	332 2 JN0067	pregnancy-specific
34	26	89.7	333 2 A43354	pregnancy-specific
35	26	89.7	335 2 A33514	pregnancy-specific
36	26	89.7	335 2 H43354	pregnancy-specific
37	26	89.7	335 2 B33251	non-specific cross-
38	26	89.7	335 2 C54312	pregnancy-specific
39	26	89.7	336 2 C27658	pregnancy-specific
40	26	89.7	348 2 T26447	hypothetical prote
41	26	89.7	352 2 I73374	pregnancy-specific
42	26	89.7	374 2 T43799	proteasome protein
43	26	89.7	389 2 JN0610	probable transcrip
44	26	89.7	395 2 D43354	pregnancy-specific
45	26	89.7	397 2 C43354	pregnancy-specific

ALIGNMENTS

RESULT 1
G90774
hypothetical protein BCs1167 (imported) - Escherichia coli (strain O157:H7, substrain
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision: 18-Jul-2001 #text_change: 18-Jul-2001
C/Accession: G90774
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C
gasaewara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g
A/Reference number: A96293; MUID:21156231; PMID:11258796
A/Accession: G90774
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-95 <HAY>
A/Cross-references: GS:BA000007; PIDN:BA34590.1; PID:G13360627; GSPDB:GN00154
A/Experimental source: strain O157:H7, substrain RMD 0509552
C/Genetics:
A/Gene: BCs1167

Query Match 100.0%; Score 29; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTMH 5
|||
DB 30 SYTMH 34

RESULT 2
S17230
Ig heavy chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 21-Nov-1993 #sequence_revision: 10-Nov-1995 #text_change: 06-Jun-1997
C/Accession: S17230
R/Lackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A/Title: Making antibody fragments using phage display libraries.
A/Reference number: S17230; MUID:91326098; PMID:1907718
A/Accession: S17230
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-96 <CLA>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F18-91/Domains: immunoglobulin homology <IMM>

Query Match 100.0%; Score 29; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTMH 5

GenCore version 5.1.4_P5_4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:56:17 ; Search time 3.96491 Seconds
(without alignments)
168.037 Million cell updates/sec

Title: US-09-644-668A-27

Perfect score: 29

Sequence: 1 SYTM 5

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

To: Number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

A-Geneseq_101002:*

1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	29	100.0	5	22	AAW90315
3	29	100.0	78	23	AAW90315
4	29	100.0	114	13	AAW90315
5	29	100.0	114	13	AAW90315
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8	29	100.0	118	22	AAW90315
9	29	100.0	118	22	AAW90315
10	29	100.0	118	22	AAW90315

11	29	100.0	120	17	AAW90315
12	29	100.0	124	20	AAW90315
13	29	100.0	135	13	AAW90315
14	29	100.0	139	19	AAW90315
15	29	100.0	139	19	AAW90315
16	29	100.0	214	20	AAW90315
17	29	100.0	279	17	AAW90315
18	29	100.0	296	20	AAW90315
19	29	100.0	34	22	AAW90315
20	29	100.0	34	22	AAW90315
21	29	100.0	37	22	AAW90315
22	29	100.0	56	21	AAW90315
23	29	100.0	77	23	AAW90315
24	29	100.0	83	22	AAW90315
25	29	100.0	112	22	AAW90315
26	29	100.0	122	12	AAW90315
27	29	100.0	125	21	AAW90315
28	29	100.0	144	11	AAW90315
29	29	100.0	166	20	AAW90315
30	29	100.0	167	22	AAW90315
31	29	100.0	183	22	AAW90315
32	29	100.0	208	20	AAW90315
33	29	100.0	228	16	AAW90315
34	29	100.0	228	19	AAW90315
35	29	100.0	238	21	AAW90315
36	29	100.0	248	11	AAW90315
37	29	100.0	281	21	AAW90315
38	29	100.0	281	21	AAW90315
39	29	100.0	315	22	AAW90315
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41	29	100.0	326	22	AAW90315
42	29	100.0	326	22	AAW90315
43	29	100.0	335	21	AAW90315
44	29	100.0	335	21	AAW90315
45	29	100.0	399	22	AAW90315

ALIGNMENTS

RESULT 1	AAW90315	standard; Protein; 5 AA.
ID	AAW90315	
XX	AAW90315	
AC	AAW90315	
DT	07-SEP-1999	(first entry)
XX		
DE	Human anti-idiotypic antibody heavy chain protein CDRI region 2.	
KW	Antibody; GPIIb/IIIa; human; auto-antibody; anti-idiotypic; diagnosis;	
KW	blood platelet membrane protein; predisposition; prevention; treatment;	
KW	autoimmune thrombocytopenic purpura; AITP; fibrinogen binding; thrombi;	
XX	thrombocyte; cardiac infarction; pulmonary embolism; heavy chain; CDRI.	
OS	Homo sapiens.	
XX		
PN	WO985619-A1.	
XX		
PD	10-DEC-1998.	
XX		
PF	05-JUN-1998;	98WO-EP03397.
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PR	08-MAY-1998;	98DE-1020663.
PR	06-JUN-1997;	97DE-1023904.
PR	12-DEC-1997;	97DE-1055227.
XX		
PA	(ASAT-) ASAT AG APPLIED SCI & TECHNOLOGY.	
PI	Berchold P, Escher RFA;	
XX		
DR	WPI; 1999-105496/09.	
XX		

Humanised M291 ant
Human anti-GPIIb/I
Humanised anti-Fac
Humanised heavy ch
Heavy chain variab
Mab Fab13B5 heavy
Humanised M291 ant
L. bimastus plasm
Novel human diagno
Human polypeptide
Human immune/haema
Arabidopsis thalia
Staphylococcus epi
Human immune/haema
Novel human secrec
Pregnancy-specific
Human secreted pro
N-terminal of SPI-
Chlamydia pneumoni
Human secreted pro
Novel human diagno
C. trachomatis lip
Tomato TGEPR2 ethy
Tomato ethylene re
Caenorhabditis ele
SPI-like protein e
Putative polynsat
Potential polynsat
Amino acid sequenc
Human polypeptide.
Human polypeptide.
Human polypeptide.
Human transmembran
Novel human diagno
Drosophila melanog

CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/098,244
FILING DATE: 17-JUN-1998
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/889,291
FILING DATE: 08-JUL-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/01835
FILING DATE: 08-JUL-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9614292.2
FILING DATE: 08-JUL-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9624880.2
FILING DATE: 29-NOV-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9712818.5
FILING DATE: 18-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/34800
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-098-244-8

Query Match 89.7%; Score 26; DB 4; Length 32;
Best Local Similarity 80.0%; Pred. No. 20;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYTMH 5
Db 9 SYTMH 13

RESULT 8
US-09-375-314-8
Sequence 8, Application US/09375314
Patent No. 6342588
GENERAL INFORMATION:
APPLICANT: Osbourn, Jane K
APPLICANT: Derbyshire, Elaine J
APPLICANT: McCafferty, John G
APPLICANT: Vaughan, Brian J
APPLICANT: Johnson, Kevin S
TITLE OF INVENTION: Labelling and selection of molecules
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIT: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/375,314
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/889,291
FILING DATE: 08-JUL-1997
APPLICATION NUMBER: PCT/GB97/01835
FILING DATE: 08-JUL-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9614292.2
FILING DATE: 08-JUL-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9624880.2
FILING DATE: 29-NOV-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9712818.5
FILING DATE: 18-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/34063
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-375-314-8

Query Match 89.7%; Score 26; DB 4; Length 32;
Best Local Similarity 80.0%; Pred. No. 20;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYTMH 5
Db 9 SYTMH 13

RESULT 9
US-09-134-001C-2990
Sequence 2990, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIORITY APPLICATION NUMBER: US 60/064,964
PRIORITY FILING DATE: 1997-11-08
PRIORITY APPLICATION NUMBER: US 60/055,779
PRIORITY FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 2990
LENGTH: 77
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2990

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Best Local Similarity 80.0%; Pred. No. 49;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTMH 5
Db 62 SYTMH 66
RESULT 10
5169835-12

TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-656-586-8

Query Match 100.0%; Score 29; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTMH 5
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DB 50 SYTMH 54

RESULT 5

US-397-411-13
Inventor: 13, Application US/08397411
Patent No. 6129914

GENERAL INFORMATION:

APPLICANT: Weiner, George
APPLICANT: Gingrich, Roger
APPLICANT: Link, Brian
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Bispecific Antibody Effective to Treat
TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,411
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/859,583
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-004901
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 279 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-397-411-13

Query Match 100.0%; Score 29; DB 3; Length 279;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTMH 5
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DB 31 SYTMH 35

RESULT 6

US-08-889-291-8
Sequence 8, Application US/08889291
Patent No. 5994519

GENERAL INFORMATION:

APPLICANT: Osbourn, Jane K.
APPLICANT: Derbyshire, Elaine J
APPLICANT: McCafferty, John G
APPLICANT: Vaughan, Tristan J
APPLICANT: Johnson, Kevin S
TITLE OF INVENTION: Labelling and selection of molecules
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/889,291
FILING DATE: 08-JUL-1997
CLASSIFICATION: 16/00, A61K 39/395
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/01835
FILING DATE: 08-JUL-1997
APPLICATION NUMBER: GB 9614292.2
FILING DATE: 08-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9624880.2
FILING DATE: 29-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9712818.5
FILING DATE: 18-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: David M. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/34063
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-889-291-8

Query Match 89.7%; Score 26; DB 2; Length 32;
Best Local Similarity 80.0%; Pred. No. 20;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTMH 5
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DB 9 SYTMH 13

RESULT 7

US-09-098-244-8
Sequence 8, Application US/09098244
Patent No. 6180316

GENERAL INFORMATION:

APPLICANT: Osbourn, Jane K.
APPLICANT: Derbyshire, Elaine J
APPLICANT: McCafferty, John G
APPLICANT: Vaughan, Tristan J
APPLICANT: Johnson, Kevin S
TITLE OF INVENTION: Labelling and selection of molecules
NUMBER OF SEQUENCES: 36

QY 1 SYTMH 5
|||
Db 31 SYTMH 35

RESULT 2

US-08-397-411-11

Sequence 11, Application US/08397411

Patent No. 6129914

GENERAL INFORMATION:

APPLICANT: Weiner, George

APPLICANT: Gingrich, Roger

APPLICANT: Link, Brian

APPLICANT: Tso, J. Yun

TITLE OF INVENTION: Bispesific Antibody Effective to Treat

TITLE OF INVENTION: B-Cell Lymphoma and Cell Line

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew

STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/397,411

FILING DATE: 01-MAR-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/859,583

FILING DATE: 27-MAR-1992

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 011823-004901

TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 120 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-397-411-11

Query Match 100.0%; Score 29; DB 3; Length 120;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTMH 5
|||
Db 31 SYTMH 35

RESULT 3
US-08-656-586-4
Sequence 4, Application US/08656586
Patent No. 5834597
GENERAL INFORMATION:
APPLICANT: Tso, J. Yun
APPLICANT: Cole, Michael S.
APPLICANT: Anasetti, Claudio
TITLE OF INVENTION: Mutated No. 5834597activating IgG2 Domains and
TITLE OF INVENTION: Anti-CD3 Antibodies Incorporating the Same
NUMBER OF SEQUENCES: 13

Query Match 100.0%; Score 29; DB 3; Length 120;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTMH 5
|||
Db 31 SYTMH 35

RESULT 4
US-08-656-586-8
Sequence 8, Application US/08656586
Patent No. 5834597
GENERAL INFORMATION:
APPLICANT: Tso, J. Yun
APPLICANT: Cole, Michael S.
APPLICANT: Anasetti, Claudio
TITLE OF INVENTION: Mutated No. 5834597activating IgG2 Domains and
TITLE OF INVENTION: Anti-CD3 Antibodies Incorporating the Same
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/656,586
FILING DATE: 31-MAY-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joseph O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 11823-007210US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/656,586

FILING DATE: 31-MAY-1996

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Liebeschuetz, Joseph O.

REGISTRATION NUMBER: 37,505

REFERENCE/DOCKET NUMBER: 11823-007210US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 139 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-656-586-4

Query Match 100.0%; Score 29; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTMH 5
|||
Db 50 SYTMH 54

RESULT 4
US-08-656-586-8
Sequence 8, Application US/08656586
Patent No. 5834597
GENERAL INFORMATION:
APPLICANT: Tso, J. Yun
APPLICANT: Cole, Michael S.
APPLICANT: Anasetti, Claudio
TITLE OF INVENTION: Mutated No. 5834597activating IgG2 Domains and
TITLE OF INVENTION: Anti-CD3 Antibodies Incorporating the Same
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/656,586
FILING DATE: 31-MAY-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joseph O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 11823-007210US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

Query Match 100.0%; Score 29; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTMH 5
|||
Db 50 SYTMH 54

RESULT 4
US-08-656-586-8
Sequence 8, Application US/08656586
Patent No. 5834597
GENERAL INFORMATION:
APPLICANT: Tso, J. Yun
APPLICANT: Cole, Michael S.
APPLICANT: Anasetti, Claudio
TITLE OF INVENTION: Mutated No. 5834597activating IgG2 Domains and
TITLE OF INVENTION: Anti-CD3 Antibodies Incorporating the Same
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/656,586
FILING DATE: 31-MAY-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joseph O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 11823-007210US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

Query Match 100.0%; Score 29; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTMH 5
|||
Db 50 SYTMH 54

RESULT 4
US-08-656-586-8
Sequence 8, Application US/08656586
Patent No. 5834597
GENERAL INFORMATION:
APPLICANT: Tso, J. Yun
APPLICANT: Cole, Michael S.
APPLICANT: Anasetti, Claudio
TITLE OF INVENTION: Mutated No. 5834597activating IgG2 Domains and
TITLE OF INVENTION: Anti-CD3 Antibodies Incorporating the Same
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/656,586
FILING DATE: 31-MAY-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joseph O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 11823-007210US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

Query Match 100.0%; Score 29; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYTMH 5
|||
Db 50 SYTMH 54

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 17:15:40 ; Search time 1.2807 Seconds

(without alignments)
114,870 Million cell updates/sec

Title: US-09-644-668A-27

Perfect score: 29

Sequence: 1 SYTMH 5

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

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Total number of hits satisfying chosen parameters: 262574

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/6CTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfilee1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	120	3	US-08-397-411-10 Sequence 10, Appl
2	29	100.0	120	3	US-08-397-411-11 Sequence 11, Appl
3	29	100.0	139	2	US-08-656-586-4 Sequence 4, Appl
4	29	100.0	139	2	US-08-656-586-8 Sequence 8, Appl
5	29	100.0	279	3	US-08-397-411-13 Sequence 13, Appl
6	26	89.7	32	2	US-08-889-291-8 Sequence 8, Appl
7	26	89.7	32	4	US-09-098-244-8 Sequence 8, Appl
8	26	89.7	32	4	US-09-375-314-8 Sequence 8, Appl
9	26	89.7	77	4	US-09-134-001C-2990 Sequence 2990, Ap
10	26	89.7	122	6	5169835-12 Patent No. 5169835
11	26	89.7	143	6	5169835-18 Patent No. 5169835
12	26	89.7	144	6	5169835-8 Patent No. 5169835
13	26	89.7	228	2	US-08-484-101B-40 Sequence 40, Appl
14	26	89.7	228	4	US-08-714-524D-40 Sequence 40, Appl
15	26	89.7	238	4	US-09-145-828A-13 Sequence 13, Appl
16	26	89.7	248	6	5169835-15 Patent No. 5169835
17	26	89.7	315	4	US-09-434-774-16 Sequence 16, Appl
18	26	89.7	406	2	US-08-222-719-1 Sequence 1, Appl
19	26	89.7	406	2	US-08-470-925-1 Sequence 1, Appl
20	26	89.7	406	2	US-08-471-613-1 Sequence 1, Appl
21	26	89.7	406	5	PCT-US93-10443-1 Patent No. 5169835
22	26	89.7	419	6	5169835-2 Patent No. 5169835
23	26	89.7	424	6	5169835-6 Patent No. 5169835
24	26	89.7	490	4	US-09-292-225-41 Sequence 41, Appl
25	26	89.7	505	4	US-09-041-075A-8 Sequence 35, Appl
26	26	89.7	509	4	US-09-292-225-35 Sequence 35, Appl
27	26	89.7	509	4	US-09-292-225-38 Sequence 38, Appl

28	26	89.7	536	4	US-09-292-225-21 Sequence 21, Appl
29	26	89.7	555	4	US-09-292-225-15 Sequence 15, Appl
30	26	89.7	555	4	US-09-292-225-18 Sequence 18, Appl
31	25	86.2	23	4	US-09-292-225-9 Sequence 9, Appl
32	25	86.2	54	4	US-09-516-352A-2 Sequence 2, Appl
33	25	86.2	67	1	US-08-162-102C-37 Sequence 37, Appl
34	25	86.2	85	2	US-08-480-229C-3 Sequence 3, Appl
35	25	86.2	85	2	US-08-659-235C-3 Sequence 3, Appl
36	25	86.2	111	1	US-08-111-939-23 Sequence 23, Appl
37	25	86.2	117	4	US-08-525-539A-76 Sequence 76, Appl
38	25	86.2	117	4	US-08-525-539A-78 Sequence 78, Appl
39	25	86.2	118	1	US-08-491-845-6 Sequence 6, Appl
40	25	86.2	118	1	US-08-491-845-14 Sequence 14, Appl
41	25	86.2	118	2	US-08-116-247-10 Sequence 10, Appl
42	25	86.2	118	3	US-08-545-809A-125 Sequence 125, Appl
43	25	86.2	119	2	US-08-303-569B-11 Sequence 11, Appl
44	25	86.2	119	2	US-08-303-569B-12 Sequence 12, Appl
45	25	86.2	119	2	US-08-303-569B-13 Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-08-397-411-10
Sequence 10, Application US/08397411
Patent No. 6129914
GENERAL INFORMATION:
APPLICANT: Weiner, George
APPLICANT: Gingrich, Roger
APPLICANT: Link, Brian
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Bispesific Antibody Effective to Treat
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,411
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/859,583
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-004901
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-397-411-10
Query Match 100.0%; Score 29; DB 3; Length 120;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

RESULT 2

US-08-488-113B-150

Sequence 150, Application US/08488113B
Patent No. 5744580

GENERAL INFORMATION:

APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.

APPLICANT: Studnika, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

TITLE OF INVENTION: Proteins

NUMBER OF SEQUENCES: 169

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/488,113B

FILING DATE: 07-JUN-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/425,336

FILING DATE: 18-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A

TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155

TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 150:

SEQUENCE CHARACTERISTICS:

LENGTH: 108 amino acids

TYPE: amino acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-488-113B-150

Query Match 89.1%; Score 49; DB 1; Length 108;

Best Local Similarity 91.7%; Pred. No. 0.031;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Patent No. 5756699

GENERAL INFORMATION:

APPLICANT: Better, Marc D.

APPLICANT: Carroll, Stephen F.

APPLICANT: Studnika, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

TITLE OF INVENTION: Proteins

NUMBER OF SEQUENCES: 169

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,484B

FILING DATE: 07-JUN-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/425,336

FILING DATE: 18-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A

TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155

TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 150:

SEQUENCE CHARACTERISTICS:

LENGTH: 108 amino acids

TYPE: amino acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-477-484B-150

Query Match 89.1%; Score 49; DB 1; Length 108;

Best Local Similarity 91.7%; Pred. No. 0.031;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 89.1%; Score 49; DB 1; Length 108;

Best Local Similarity 91.7%; Pred. No. 0.031;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Wed Apr 16 17:34:48 2003

US-09-644-668a-24. rat

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using SW model

Run on: April 16, 2003, 17:15:40 / Search time 3.07368 Seconds
(without alignments)
114.870 Million cell updates/sec

Title: US-09-644-668a-24

Perfect score: 55

Sequence: 1 RASQSVSSSYLA 12

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	89.1	107	2	US-08-652-558-49
2	49	89.1	108	1	US-08-488-113B-150
3	49	89.1	108	1	US-08-477-484B-150
4	49	89.1	108	2	US-08-646-360-150
5	49	89.1	108	2	US-08-232-081B-42
6	49	89.1	108	4	US-08-839-765-150
7	49	89.1	108	4	US-09-136-389-150
8	49	89.1	108	4	US-09-610-838-150
9	49	89.1	109	4	US-09-025-769B-16
10	49	89.1	110	4	US-09-025-769B-10
11	49	89.1	110	4	US-09-025-769B-47
12	49	89.1	116	1	US-08-053-131-183
13	49	89.1	116	2	US-08-096-762-183
14	49	89.1	116	4	US-09-042-353-46
15	49	89.1	116	4	US-08-758-417A-311
16	49	89.1	150	4	US-08-862-124-17
17	49	89.1	287	4	US-08-862-124-17
18	49	89.1	304	4	US-08-862-124-14
19	48	87.3	108	4	US-09-240-274-178
20	46	83.6	109	1	US-08-276-852-147
21	46	83.6	109	1	US-08-899-575-147
22	46	83.6	109	1	US-08-899-575-147
23	46	83.6	109	5	PCT-US95-08743-147
24	45	81.8	112	1	US-08-276-852-151
25	45	81.8	112	1	US-08-899-575-151
26	45	81.8	112	1	US-08-899-575-151
27	45	81.8	112	5	PCT-US95-08743-151

28	44	80.0	129	2	US-08-480-774A-4	Sequence 4, Appl.
29	43	78.2	107	1	US-08-276-852-87	Sequence 87, Appl
30	43	78.2	107	1	US-08-899-575-87	Sequence 87, Appl
31	43	78.2	107	1	US-08-899-575-87	Sequence 87, Appl
32	43	78.2	107	5	PCT-US95-08743-87	Sequence 87, Appl
33	42	76.4	57	1	US-08-162-102C-38	Sequence 38, Appl
34	42	76.4	105	1	US-08-276-852-93	Sequence 93, Appl
35	42	76.4	105	1	US-08-899-575-93	Sequence 93, Appl
36	42	76.4	105	1	US-08-899-575-93	Sequence 93, Appl
37	42	76.4	105	5	PCT-US95-08743-93	Sequence 93, Appl
38	42	76.4	108	1	US-08-276-852-86	Sequence 86, Appl
39	42	76.4	108	1	US-08-899-575-86	Sequence 86, Appl
40	42	76.4	108	1	US-08-899-575-86	Sequence 86, Appl
41	42	76.4	108	5	PCT-US95-08743-86	Sequence 86, Appl
42	42	76.4	109	1	US-08-162-102C-23	Sequence 23, Appl
43	42	76.4	109	5	PCT-US93-08786-23	Sequence 23, Appl
44	42	76.4	111	1	US-08-276-852-149	Sequence 149, App
45	42	76.4	111	1	US-08-899-575-149	Sequence 149, App

ALIGNMENTS

RESULT 1
US-08-652-558-49
Sequence 49, Application US/08652558
Patent No. 5861155
GENERAL INFORMATION:
APPLICANT: LIN, AUGUSTINE YEE-THARN
TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSER: BANNER & MITCOFF
STREET: 75 STATE STREET, 23RD FLOOR
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,558
FILING DATE: JUNE 6, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB94/00387
FILING DATE: NOVEMBER 21, 1994
ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, LEON R.
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: 95,497-L
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-9110
TELEFAX: 617-345-9111
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-652-558-49
Query Match: 89.1%, Score 49; DB 2; Length 107;
Best Local Similarity: 91.7%; Pred. No. 0.03;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 RASQSVSSSYLA 12
Db 24 RASQSVSSSYLA 35

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 38
LENGTH: 12
TYPE: PRT
ORGANISM: Homo sapiens
US-09-828-708-38

Query Match 89.1%; Score 49; DB 10; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.013;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
|||||
DB 1 RASQSVSSSYLA 12

RESULT 3
US-09-828-708-40
Sequence 40; Application US/09828708
Pat No. US20020146753A1
GENERAL INFORMATION:
APPLICANT: Ditzel, H.
APPLICANT: Burton, D.
APPLICANT: Schaller, M.
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particl
FILE REFERENCE: 1361.005US1
CURRENT APPLICATION NUMBER: US/09/828,708
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 40
LENGTH: 12
TYPE: PRT
ORGANISM: Homo sapiens
US-09-828-708-40

Query Match 89.1%; Score 49; DB 10; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.013;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
|||||
DB 1 RASQSVSSSYLA 12

RESULT 4
US-09-828-708-41
Sequence 41; Application US/09828708
Patent No. US20020146753A1
GENERAL INFORMATION:
APPLICANT: Ditzel, H.
APPLICANT: Burton, D.
APPLICANT: Schaller, M.
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particl
FILE REFERENCE: 1361.005US1
CURRENT APPLICATION NUMBER: US/09/828,708
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 41
LENGTH: 12
TYPE: PRT
ORGANISM: Homo sapiens
US-09-828-708-41

Query Match 89.1%; Score 49; DB 10; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.013;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 1 RASQSVSSSYLA 12

RESULT 5
US-09-828-708-42
Sequence 42; Application US/09828708
Patent No. US20020146753A1
GENERAL INFORMATION:
APPLICANT: Ditzel, H.
APPLICANT: Burton, D.
APPLICANT: Schaller, M.
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particl
FILE REFERENCE: 1361.005US1
CURRENT APPLICATION NUMBER: US/09/828,708
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 42
LENGTH: 12
TYPE: PRT
ORGANISM: Homo sapiens
US-09-828-708-42

Query Match 89.1%; Score 49; DB 10; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.013;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
|||||
DB 1 RASQSVSSSYLA 12

RESULT 6
US-10-125-687-23
Sequence 23; Application US/10125687
Publication No. US20030054407A1
GENERAL INFORMATION:
APPLICANT: Luo, Peter
TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
FILE REFERENCE: 26050-705
CURRENT APPLICATION NUMBER: US/10/125,687
CURRENT FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 23
LENGTH: 74
TYPE: PRT
ORGANISM: Homo sapiens
US-10-125-687-23

Query Match 89.1%; Score 49; DB 9; Length 74;
Best Local Similarity 91.7%; Pred. No. 0.076;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
|||||
DB 17 RASQSVSSSYLA 28

RESULT 7
US-10-025-687-23
Sequence 23; Application US/10025687
Patent No. US20020142255A1
GENERAL INFORMATION:
APPLICANT: Luo, Peter
TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
FILE REFERENCE: 26050-705
CURRENT APPLICATION NUMBER: US/10/025,687
CURRENT FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 23

Wed, Apr 16 17:34:49 2003

us-09-644-668a-24.rapb

P

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using SW model

Run on: April 16, 2003, 17:21:54 ; Search time 3.53684 Seconds

(without alignments)
256.547 Million cell updates/sec

Title: US-09-644-668a-24

Sequence: 1 RASQVSSSYLA 12

Scoring table: BLOSUM62

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To: Number of hits satisfying chosen parameters: 288829

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	89.1	12	9	US-10-001-934-62
2	49	89.1	12	10	US-09-828-708-38
3	49	89.1	12	10	US-09-828-708-40
4	49	89.1	12	10	US-09-828-708-41
5	49	89.1	12	10	US-09-828-708-42
6	49	89.1	12	10	US-10-125-687-23
7	49	89.1	12	10	US-10-025-687-23
8	49	89.1	12	10	US-10-194-975-82
9	49	89.1	12	10	US-09-828-708-6
10	49	89.1	12	10	US-09-828-708-3
11	49	89.1	12	10	US-09-828-708-5
12	49	89.1	12	10	US-09-828-708-7
13	49	89.1	12	10	US-09-828-708-4
14	49	89.1	12	10	US-09-828-708-21
15	49	89.1	12	10	US-10-125-687-10
16	49	89.1	12	10	US-10-025-687-10
17	49	89.1	12	10	US-10-001-934-40
18	49	89.1	12	10	US-09-828-708-5
19	49	89.1	12	10	US-09-828-708-4

20	49	89.1	252	9	US-09-880-748-1534	Sequence 1534, Ap
21	49	89.1	287	9	US-09-782-397-17	Sequence 17, Ap
22	49	89.1	304	9	US-09-782-397-14	Sequence 14, Ap
23	48	87.3	108	9	US-09-848-798-178	Sequence 178, Ap
24	48	87.3	245	9	US-09-880-748-1896	Sequence 1896, Ap
25	46	83.6	96	9	US-10-194-975-88	Sequence 88, Ap
26	46	83.6	107	8	US-08-844-215-8	Sequence 8, Ap
27	44	80.0	12	9	US-09-977-797A-24	Sequence 24, Ap
28	44	80.0	96	9	US-10-194-975-83	Sequence 83, Ap
29	44	80.0	253	9	US-09-880-748-1534	Sequence 1499, Ap
30	43	78.2	236	10	US-09-859-053-34	Sequence 34, Ap
31	43	78.2	254	9	US-09-880-748-905	Sequence 905, Ap
32	42	76.4	106	8	US-08-844-215-14	Sequence 14, Ap
33	40	72.7	109	9	US-09-144-886-91	Sequence 91, Ap
34	40	72.7	109	9	US-10-141-908-8	Sequence 8, Ap
35	40	72.7	146	9	US-09-925-299-776	Sequence 776, Ap
36	40	72.7	146	10	US-09-925-299-776	Sequence 776, Ap
37	39	70.9	11	9	US-09-968-561A-298	Sequence 298, Ap
38	39	70.9	11	10	US-09-192-854-170	Sequence 170, Ap
39	39	70.9	88	10	US-09-905-243-10	Sequence 30, Ap
40	39	70.9	95	9	US-10-194-975-91	Sequence 91, Ap
41	39	70.9	95	9	US-10-194-975-92	Sequence 92, Ap
42	39	70.9	107	8	US-08-844-215-10	Sequence 10, Ap
43	39	70.9	236	10	US-09-859-053-38	Sequence 38, Ap
44	39	70.9	249	9	US-09-880-748-1035	Sequence 1035, Ap
45	38.5	70.0	95	9	US-10-194-975-86	Sequence 86, Ap

ALIGNMENTS

RESULT 1
US-10-001-934-62
Sequence 62, Application US/10001934
Publication No. US20030032782A1
GENERAL INFORMATION:
APPLICANT: NAGY, ZOLTAN
TITLE OF INVENTION: HUMAN PEPTIDES/PROTEINS CAUSING OR LEADING TO THE
FILE OF INVENTION: KILLING OF CELLS INCLUDING LYMPHOID TUMOR CELLS
FILE REFERENCE: GPOG-P01-003
CURRENT APPLICATION NUMBER: US/10/001.934
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 62
LENGTH: 12
TYPE: PRT
ORGANISM: Homo sapiens
US-10-001-934-62

Query Match 89.1%; Score 49; DB 9; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.013;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQVSSSYLA 12
DB 1 RASQVSSSYLA 12

RESULT 2
US-09-828-708-38
Sequence 38, Application US/09828708
Patent No. US20020146753A1
GENERAL INFORMATION:
APPLICANT: Ditzel, H.
APPLICANT: Burton, D.
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their parti
FILE REFERENCE: 1361.005US1
CURRENT APPLICATION NUMBER: US/09/828, 708
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 123

PT Novel human sequence antibody that binds to human cytotoxic T
 CC lymphocyte associated antigen-4, useful for inducing, augmenting or
 PT prolonging immune response to antigen or for suppressing immune
 CC response in patient
 XX
 PS Claim 30; Page 99; 127pp; English.

CC AAB67490-99 and AAB67501-06 represents complementarity determining
 CC regions (CDRs) of human antibodies. The antibodies specifically bind to
 CC human cytotoxic T lymphocyte associated antigen-4 (CTLA-4). Such
 CC antibodies are used in methods for inducing, augmenting or prolonging
 CC an immune response to an antigen in a patient, where the antibodies
 CC block binding of human CTLA-4 to human B7 ligands. The antibodies are
 CC also useful for treating autoimmune disease in a subject caused or
 CC exacerbated by increased activity of T cells and for treating prostate
 CC cancer, melanoma or epithelial cancer. A polyvalent or polyclonal
 CC antibody preparation comprising two antibodies of the invention are
 CC useful for suppressing a immune response in a patient. They are used for
 CC treating cancer, infectious diseases and promoting beneficial autoimmune
 CC actions for the treatment of diseases with inflammatory or allergic
 CC components. The polyvalent or polyclonal preparations are useful for
 CC treating autoimmune diseases such as rheumatoid arthritis, myasthenia
 CC gravis and lupus erythematosus, multiple sclerosis, insulin-dependent
 CC diabetes mellitus, transplant rejection, and inflammation, graft versus
 CC host disease.

CC Sequence 12 AA;

Query Match 100.0%; Score 55; DB 22; Length 12;

Best Local Similarity 100.0%; Pred. No. 0.00018;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RASQSVSSSYLA 12
 DB 1 RASQSVSSSYLA 12

RESULT 2

AAR15375 standard; Protein; 12 AA.

XX AAR15375;

XX 05-MAR-1992. (first entry)

XX IGM-RF GLO.

XX rheumatoid factor; RF; antigen; CDR; IGM.

XX Synthetic.

XX US068177-A.

XX 26-NOV-1991.

XX 05-AUG-1985; 85US-0762698.

XX 05-AUG-1985; 85US-0762698.

XX 28-DEC-1983; 83US-0566172.

XX (SCRI-) SCRIPPS CLINIC RES.

XX Carson DA, Fong S, Chen PP;

XX WPI; 1991-368612/50.

XX Synthetic polypeptide(s) for inducing anti-idiotypic antibodies -
 PT useful for treating auto immune-, endocrine- and
 PT rheumatic-diseases and myasthenia gravis

XX Claim 10; Page 42; 44pp; English.

XX Three rabbits were inoculated with two s.c. injections of PGL1

CC (synthetic peptide) conjugated to KLH as an immunogen, and their
 CC sera were analysed for anti-peptide antibody activity by ELISA.
 CC All three immunised rabbits produced anti-PGL1 antibody. Antisera
 CC drawn from a rabbit on two different days reacted significantly with
 CC the corresp. intact IGM-RF GLO.
 CC See also AAR15365-74 and AAR15375.

CC Sequence 12 AA;

Query Match 89.1%; Score 49; DB 12; Length 12;

Best Local Similarity 91.7%; Pred. No. 0.003;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RASQSVSSSYLA 12
 DB 1 RASQSVSSSYLA 12

RESULT 3

AAU83718 standard; Peptide; 12 AA.

XX AAU83718;

XX 08-MAY-2002 (first entry)

XX MS-GPC-6 light chain variable region CDR1 sequence.

XX Human; antibody-based antigen; HLA-DR; CDR; antibody;
 XX human leukocyte antigen; cell proliferative disorder; lymphoma;
 XX HNC class II antigen disorder; lymphoma; B cell lymphoma; leukaemia;
 XX acute myeloid leukaemia; rheumatoid arthritis; multiple sclerosis;
 XX Grave's disease; insulin-dependent diabetes; transplant rejection;
 XX systemic lupus erythematosus; graft vs. host disease; myasthenia gravis;
 XX irritable bowel disease; Sjogren's syndrome; interleukin-2 secretion;
 XX IL-2; MS-GPC; complementarity determining region.

XX Homo sapiens.

XX WO200187337-A1.

XX 22-NOV-2001.

XX 14-MAY-2001; 2001WO-US15625.

XX 12-MAY-2000; 2000EP-0110065.

XX 06-OCT-2000; 2000US-238492P.

XX (GPCB-) GPC BIOTECH AG.

XX (MORP-) MORPHOSYS AG.

XX Nagy Z, Brunner C, Teaser M, Thomassen-Wolf B;

XX WPI; 2002-075288/10.

XX Polypeptide compositions which bind to cell surface epitopes, which in
 PT multivalent form kills lymphoid tumour cells and in monovalent form
 PT causes immunosuppression or inhibits activation of lymphocytes

XX Example 4; Page 66; 150pp; English.

XX The invention relates to a composition which includes a polypeptide
 CC or a multivalent polypeptide comprising one or more
 CC antibody-based antigen-binding domain of human composition
 CC with binding specificity for an antigen expressed on surface of a
 CC human cell, especially HLA-DR (human leukocyte antigen DR), where
 CC treating cells expressing HLA-DR with the multivalent polypeptide causes
 CC or leads to killing of cells without need of cytotoxic entities or
 CC immunological mechanisms. Also included are the nucleic acid
 CC encoding the polypeptide, a vector comprising the nucleic acid and a host
 CC cell harbouring vector or nucleic acid. The polypeptide (optionally
 CC linked to cytotoxic or immunogenic agent), the nucleic acid and the host
 CC cell are useful for preparing a pharmaceutical preparation for the

Wed Apr 16 17:34:47 2003

us-09-644-668a-24.rag

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using SW model

Run on: April 16, 2003, 16:56:17 ; Search time 9.51579 Seconds

(without alignments)
168.037 Million cell updates/sec

Title: US-09-644-668a-24

Sequence: 1 RASQGVGSXYLA 12

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	55	100.0	12 22	AA67493 Human light chain
2	49	89.1	12 12	AA67493 IGM-RF glo. Synth
3	49	89.1	12 23	AA67493 MS-GPC-6 light cha
4	49	89.1	12 23	AA67493 HLA-DR-specific pr
5	49	89.1	12 23	AA67493 HLA-DR-specific pr
6	49	89.1	12 23	AA67493 HLA-DR-specific pr
7	49	89.1	12 23	AA67493 HLA-DR-specific pr
8	49	89.1	12 23	AA67493 Human kappa III 11
9	49	89.1	101 23	AA67493 CB21E12 kappa chain
10	49	89.1	108 21	AA67493 VL component of an

11	49	89.1	108 22	AA67493 Human scFv L19 ant
12	49	89.1	108 23	AA67493 Antibody screening
13	49	89.1	109 20	AA67493 Human V kappa subg
14	49	89.1	109 22	AA67493 Human HIV-1 monoclon
15	49	89.1	109 23	AA67493 Anti-IL-4 receptor
16	49	89.1	109 23	AA67493 Anti-IL-4 and IL-1
17	49	89.1	110 18	AA67493 Human Ab light cha
18	49	89.1	110 23	AA67493 MS-GPC-6 light cha
19	49	89.1	110 23	AA67493 HLA-DR-specific pr
20	49	89.1	110 23	AA67493 HLA-DR-specific pr
21	49	89.1	110 23	AA67493 HLA-DR-specific pr
22	49	89.1	110 23	AA67493 HLA-DR-specific pr
23	49	89.1	116 14	AA67493 Human V-kappa frag
24	49	89.1	116 15	AA67493 Human V-kappa frag
25	49	89.1	116 17	AA67493 Human V-kappa frag
26	49	89.1	116 18	AA67493 Human V-kappa frag
27	49	89.1	116 19	AA67493 Human V-kappa frag
28	49	89.1	116 20	AA67493 Human V-kappa frag
29	49	89.1	129 14	AA67493 Human V-kappa frag
30	49	89.1	150 19	AA67493 Human V-kappa frag
31	49	89.1	150 22	AA67493 Human V-kappa frag
32	49	89.1	224 22	AA67493 Human V-kappa frag
33	49	89.1	224 22	AA67493 Human V-kappa frag
34	49	89.1	224 22	AA67493 Human V-kappa frag
35	49	89.1	224 22	AA67493 Human V-kappa frag
36	49	89.1	224 22	AA67493 Human V-kappa frag
37	49	89.1	224 22	AA67493 Human V-kappa frag
38	49	89.1	226 22	AA67493 Human V-kappa frag
39	49	89.1	226 22	AA67493 Human V-kappa frag
40	49	89.1	226 22	AA67493 Human V-kappa frag
41	49	89.1	226 22	AA67493 Human V-kappa frag
42	49	89.1	226 22	AA67493 Human V-kappa frag
43	49	89.1	226 22	AA67493 Human V-kappa frag
44	49	89.1	226 22	AA67493 Human V-kappa frag
45	49	89.1	226 22	AA67493 Human V-kappa frag

ALIGNMENTS

RESULT 1
ID AAB67493 standard; peptide; 12 AA.
AC AAB67493;
XX
DT 29-MAY-2001 (first entry)
XX
XX Human light chain complementarity determining region 1 (CDR1).
XX
XX Complementarity determining region; CDR; immune response; antibody;
XX cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;
XX autoimmune disease; infectious disease; inflammation; allergy;
XX rheumatoid arthritis; myasthenia gravis; lupus erythematosus;
XX multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;
XX transplant rejection; graft versus host disease.
XX
XX Homo sapiens.
XX
XX WO200114424-A2.
XX
XX 01-MAR-2001.
XX
XX 24-AUG-2000; 2000WO-US23356.
XX
XX 24-AUG-1999; 99US-0150452.
XX
XX (MEDA-) MEDAREX INC.
XX
XX Korman AJ, Halk EL, Lonberg N;
XX WPI, 2001-202933/20.
XX
XX

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RESULT 2
ID 09UL78 PRELIMINARY; PRT; 109 AA.
AC 09UL78;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OC Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT Myosin-reactive autoantibodies in rheumatic carditis and normal
RT etus.;
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035036; AADS6272.1; -.
DR HSSP; P80362; 1WTI.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGv_1.
DR NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52ECTHE197 CRC64;

Query Match 89.1%; Score 49; DB 4; Length 109;
Best Local Similarity 91.7%; Pred. No. 0.029;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQSVGSSYLA 12
Db 24 RASQSVSSSYLA 35

RESULT 3
ID P96258 PRELIMINARY; PRT; 439 AA.
AC P96258;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical protein RV0412c.
GN RV0412C OR MT0425 OR MTCY22G10.08C.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OC NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=H37RV.
RC MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Odborn J., Quail M.A., Rajandram M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RN Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COC 1551 / OSHKOSH;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

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```

RA Peterson J., DeBoy R., Dodson R., Gwin M., Haft D., Hickey B.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Blahut W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z84724; CAB06582.1; -.
DR EMBL; AE006946; AAK44649.1; -.
DR TIGR; MT0425; -.
KW Tuberculosis; RV0412c;
KW Hypothetical protein; Complete proteome.
FT CONFLICT 355 355 D -> Y (IN RBF. 2).
SQ SEQUENCE 439 AA; 47115 MW; 7B57FA98C0472465 CRC64;

Query Match 69.1%; Score 38; DB 16; Length 439;
Best Local Similarity 66.7%; Pred. No. 25;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Db 159 RASQSVSSYLA 170

QY 1 RASQSVGSSYLA 12
Db 159 RASQSVSSYLA 170

RESULT 4
ID 09B076 PRELIMINARY; PRT; 261 AA.
AC 09B076;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Gp45.
GN 45.
OS Mycobacteriophage Bxb1.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OC NCBI_TaxID=148603;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20572070; PubMed=11123671;
RA Mediavilla J., Jain S., Kriakov J., Ford M.E., Duda R.L., Jacobs W.R.,
RA Hendrix R.W., Hatfull G.F.;
RT "Genome organization and characterization of mycobacteriophage bxb1.";
RL Mol. Microbiol. 38:955-970(2000).
DR EMBL; AF271693; AAG59750.1; -.
SQ SEQUENCE 261 AA; 28704 MW; 160F6385FE4539A5 CRC64;

Query Match 67.3%; Score 37; DB 9; Length 261;
Best Local Similarity 54.5%; Pred. No. 22;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSYLA 11
Db 10 KAARSIGNSYLA 20

RESULT 5
ID 09BLB1 PRELIMINARY; PRT; 2311 AA.
AC 09BLB1;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE L5178.1.
GN L5178.1.
OS Leishmania major.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OC NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RA Wyler P.J., Sisk E., Cawthra J., Handley F., Vogt C., Robertson L.,
RA McDonagh P., Stuart K., Ivens A., Wortley E.A.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

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OM protein - protein search, using sw model

(without alignments)
201.108 Million cell updates/sec

Perfect score: 55
Sequence: 1 RASQSVGSSYL A 12

Gapop 10.0 , Gapext 0.5

To number of hits satisfying chosen parameters: 671580

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0.4

Maximum Match 100%
Listing first 45 summaries

Database :

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4:  sp.human:*
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6:  sp.mammal:*
7:  sp.mbc:*
8:  sp.organelle:*
9:  sp.phage:*
10: sp.plant:*
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12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	48	89.1	109	4	Q9UL86		Q9UL86 homo sapien
2	49	89.1	109	4	Q9UL78		Q9UL78 homo sapien
3	38	69.1	439	16	P96258		P96258 mycobacteri
4	37	67.3	261	9	Q9B076		Q9B076 mycobacteri
5	35	65.5	231	5	Q9BLB1		Q9BLB1 leishmania
6	35	63.6	316	16	Q9BK17		Q9BK17 rhizobium
7	35	63.6	378	16	Q9K6C2		Q9K6C2 caulobacter
8	35	63.6	387	16	Q9K5D0		Q9K5D0 rhizobium
9	35	63.6	387	16	Q9K5V1		Q9K5V1 rhizobium
10	35	63.6	333	16	Q9K2Q6		Q9K2Q6 ralsomonia
11	35	63.6	823	5	Q9XXS6		Q9XXS6 caenorhabdi
12	35	63.6	2179	12	Q91DM0		Q91DM0 pecunia vel
13	34	61.8	158	11	Q9R4K6		Q9R4K6 rattus norv
14	34	61.8	204	4	Q93NP6		Q93NP6 athrobacte
15	34	61.8	339	5	O17844		O17844 caenorhabdi
16	34	61.8	382	16	Q9EYPS		Q9EYPS brucella me

17	34	61.8	401	10	Q9FS87	Q9F887 solanum t.
18	34	61.8	408	10	Q9SM62	Q9sm62 pium sativi
19	34	61.8	409	10	Q9SM61	Q9sm61 pium sativi
20	34	61.8	421	16	Q8UA97	Q8ua97 agrocacteri
21	34	61.8	464	17	Q97A25	Q97a15 thermoplas
22	34	61.8	595	17	Q8TRN3	Q8trn3 methanocarr
23	34	61.8	611	16	Q9PPW9	Q9ppw9 ureaplasma
24	34	61.8	716	16	Q98J57	Q98j57 thizobium
25	34	61.8	782	4	Q96A82	Q96a82 homo sapien
26	34	61.8	863	12	Q87027	Q87027 saccharomy
27	34	61.8	1055	10	Q9SAV0	Q9sav0 aridopsis
28	35.5	60.9	107	4	Q96SA9	Q96sa9 homo sapien
29	33.5	60.9	152	16	Q9UL77	Q9ul77 homo sapien
30	33	60.0	108	10	Q98NC2	Q98nc2 thizobium
31	33	60.0	259	10	Q38730	Q38730 arum macula
32	33	60.0	282	10	Q887V3	Q887v3 oryza sativi
33	33	60.0	315	16	Q99WQ0	Q99wq0 staphylococ
34	33	60.0	363	16	Q8XK57	Q8xk57 clostridium
35	33	60.0	387	2	Q9R9S5	Q9r9s5 aeromonas p
36	33	60.0	403	1	Q9ZBL6	Q9zbl6 mycobacteri
37	33	60.0	405	5	Q95YR0	Q95yr0 leishmania
38	33	60.0	432	17	Q96TG4	Q96tg4 sulfolobus
39	33	60.0	442	16	Q9CEG6	Q9ceg6 lactococcus
40	33	60.0	446	5	Q9N3X0	Q9n3x0 caenorhabdi
41	33	60.0	469	12	Q9PEZG0	Q9pezg0 influenza a
42	33	60.0	474	10	Q9XEB9	Q9xeb9 arabidopsis
43	33	60.0	569	3	Q96UN2	Q96un2 neutrospora
44	33	60.0	693	17	Q58898	Q58898 pyrococcus
45	33	60.0	894	5	Q917V0	Q917v0 drosoophila

ALIGNMENTS

[illegible]

RP SEQUENCE FROM N.A.
 RX MEDLINE=88171307; PubMed=3127527;
 RA Klips T.J., Tomhave E., Chen P.P., Carson D.A.;
 RT "Anticentibody-associated kappa light chain variable region gene
 expressed in chronic lymphocytic leukemia with little or no somatic
 mutation. Implications for etiology and immunotherapy.";
 RL J. Exp. Med. 167:840-852(1988).
 CC -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
 AUTANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
 LEUKEMIA.
 CC PIR; P00022; K3HUA.
 DR HSP; P80362; IWT.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig_V.
 DR SMART; SM00406; IGV; 1.
 KM Immunoglobulin V region; Signal.
 FT CHAIN 1 129
 FT SIGNAL 20
 FT OMAIN 21 43 IG KAPPA CHAIN V-III REGION HAM.
 FT OMAIN 44 55 FRAMEWORK-1.
 FT OMAIN 56 70 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 71 77 FRAMEWORK-2.
 FT DOMAIN 78 109 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 110 118 FRAMEWORK-3.
 FT DOMAIN 119 129 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 43 109 JKI SEGMENT.
 FT NON TER 129 BY SIMILARITY.
 SQ SEQUENCE 129 AA; 14073 MW; D3C5529272774740 CRC64;
 Query Match 89.1%; Score 49; DB 1; Length 129;
 Best Local Similarity 91.7%; Pred. No. 0.006;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RASQSVSSSYLA 12
 DB 44 RASQSVSSSYLA 55

RESULT 3
 KV3M HUMAN STANDARD; PRT; 129 AA.
 ID KV3M_HUMAN
 AC P18136;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region HIC precursor.
 OS Homo sapiens (Human).
 OC Mammalia; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88171307; PubMed=3127527;
 RA Klips T.J., Tomhave E., Chen P.P., Carson D.A.;
 RT "Anticentibody-associated kappa light chain variable region gene
 expressed in chronic lymphocytic leukemia with little or no somatic
 mutation. Implications for etiology and immunotherapy.";
 RL J. Exp. Med. 167:840-852(1988).
 CC -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
 AUTANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
 LEUKEMIA.
 CC PIR; P00021; K3HUI.
 DR HSP; P80362; IWT.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig_V.
 DR SMART; SM00406; IGV; 1.
 KM Immunoglobulin V region; Signal.
 FT CHAIN 1 129
 FT SIGNAL 20
 FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 56 70 FRAMEWORK-2.
 FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 78 109 FRAMEWORK-3.
 FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 43 109 JKI SEGMENT.
 FT NON TER 129 BY SIMILARITY.
 SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2BB74D6 CRC64;
 Query Match 89.1%; Score 49; DB 1; Length 129;
 Best Local Similarity 91.7%; Pred. No. 0.006;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RASQSVSSSYLA 12
 DB 44 RASQSVSSSYLA 55

RESULT 4
 KV3B HUMAN STANDARD; PRT; 109 AA.
 ID KV3B_HUMAN
 AC P01620;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region SIE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=82046598; PubMed=6794615;
 RA Andrews D.W., Capra J.D.;
 RT "Amino acid sequence of the variable regions of light chains from two
 RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
 RT group.";
 RL Biochemistry 20:5816-5822(1981).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
 GLOBULIN ACTIVITY.
 CC PIR; A01892; K3HUI.
 DR HSP; P80362; IWT.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; IGV; 1.
 DR SMART; SM00406; IGV; 1.
 KM Immunoglobulin V region.
 FT DISULFID 23 89
 FT NON TER 109
 SQ SEQUENCE 109 AA; 11775 MW; 7689C3BCDD646FPB4 CRC64;
 Query Match 83.6%; Score 46; DB 1; Length 109;
 Best Local Similarity 83.3%; Pred. No. 0.021;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RASQSVSSSYLA 12
 DB 24 RASQSVSSSYLA 35

RESULT 5
 KV3F HUMAN STANDARD; PRT; 109 AA.
 ID KV3F_HUMAN
 AC P01624;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig kappa chain V-III region POW.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]

22
[1]

NCBI_18X1D=9606;
CA
RN [1]

RESULT 3

S34096

Ig kappa chain V region - human

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000

C/Accession: S34096

R/Wagner, S.D.; Luzzatto, L.

Eur. J. Immunol. 23, 391-397, 1993

A/Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed

A/Reference number: S34076; MUID:93170387; PMID:8436174

A/Accession: S34096

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-89 <KLE>

A/Cross-references: EMBL:X67180

C/Superfamily: Immunoglobulin V region; Immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

P/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 89.1%; Score 49; DB 2; Length 89;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12

Db 17 RASQSVSSSYLA 28

RESULT 4

S37520

Ig kappa chain V region (V-kappa 3) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C/Accession: S37520

R/Klein, U.; Kuipers, R.; Rajewsky, K.

Submitted to the EMBL Data Library, September 1993

A/Description: Human IGM(+) Igd(+) cells, the major B cell subset in the peripheral blood

A/Reference number: S37501

A/Accession: S37520

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-91 <KLE>

A/Cross-references: EMBL:Z26612; NID:9405682; PIDN:CAA81365.1; PID:9405683

C/Superfamily: Immunoglobulin V region; Immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Y Match

Best Local Similarity 89.1%; Score 49; DB 2; Length 91;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12

Db 7 RASQSVSSSYLA 18

RESULT 5

S67940

Ig kappa chain V region, subgroup III (clone MH52) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 20-Mar-1998

C/Accession: S67940

R/Hexham, J.M.; Furmaniak, J.; Pegg, C.; Burton, D.R.; Smith, B.R.

Autoimmunity 12, 135-141, 1992

A/Title: Cloning of a human autoimmune response: preparation and sequencing of a human a

A/Reference number: S67940; MUID:92313301; PMID:1617110

A/Accession: S67940

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-91 <HEX>

A/Cross-references: EMBL:X73852

C/Superfamily: Immunoglobulin V region; Immunoglobulin homology

Query Match

Best Local Similarity 89.1%; Score 49; DB 2; Length 91;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12

Db 5 RASQSVSSSYLA 16

RESULT 6

S37513

Ig kappa chain V region (V-kappa 3) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C/Accession: S37513

R/Klein, U.; Kuipers, R.; Rajewsky, K.

Submitted to the EMBL Data Library, September 1993

A/Description: Human IGM(+) Igd(+) cells, the major B cell subset in the peripheral blood

A/Reference number: S37501

A/Accession: S37513

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-92 <KLE>

A/Cross-references: EMBL:Z26598; NID:9405682; PIDN:CAA81352.1; PID:9405689

C/Superfamily: Immunoglobulin V region; Immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 89.1%; Score 49; DB 2; Length 92;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12

Db 7 RASQSVSSSYLA 18

RESULT 7

S37519

Ig kappa chain V region (V-kappa 3) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C/Accession: S37519

R/Klein, U.; Kuipers, R.; Rajewsky, K.

Submitted to the EMBL Data Library, September 1993

A/Description: Human IGM(+) Igd(+) cells, the major B cell subset in the peripheral blood

A/Reference number: S37501

A/Accession: S37519

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-92 <KLE>

A/Cross-references: EMBL:Z26613; NID:9405680; PIDN:CAA81366.1; PID:9405681

C/Superfamily: Immunoglobulin V region; Immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 89.1%; Score 49; DB 2; Length 92;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12

Db 7 RASQSVSSSYLA 18

RESULT 8

S37517

Ig kappa chain V region (V-kappa 3) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C/Accession: S37517

R/Klein, U.; Kuipers, R.; Rajewsky, K.

Submitted to the EMBL Data Library, September 1993

A/Description: Human IGM(+) Igd(+) cells, the major B cell subset in the peripheral

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 17:11:36 ; Search time 3.70526 Seconds
(without alignments)
311.344 Million cell updates/sec

Title: US-09-644-668a-24

Perfect score: 55

Sequence: 1 RASQSVSSSYLA 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Query Match	Length	DB	ID	Description
1	49	89.1	83	2	I30607	Ig kappa chain V-I
2	49	89.1	87	2	S16823	Ig kappa chain V-I
3	49	89.1	89	2	S34096	Ig kappa chain V-I
4	49	89.1	91	2	S37520	Ig kappa chain V-I
5	49	89.1	91	2	S67940	Ig kappa chain V-I
6	49	89.1	92	2	S37513	Ig kappa chain V-I
7	49	89.1	92	2	S37519	Ig kappa chain V-I
8	49	89.1	92	2	S37517	Ig kappa chain V-I
9	49	89.1	92	2	S37514	Ig kappa chain V-I
10	49	89.1	92	2	S37518	Ig kappa chain V-I
11	49	89.1	93	2	S37526	Ig kappa chain V-I
12	49	89.1	93	2	S37528	Ig kappa chain V-I
13	49	89.1	93	2	S37501	Ig kappa chain V-I
14	49	89.1	96	2	A30601	Ig kappa chain V-I
15	49	89.1	100	1	K3H0M1	Ig kappa chain V-I
16	49	89.1	104	2	PH0964	Ig kappa chain V-I
17	49	89.1	107	2	PH0965	Ig kappa chain V-I
18	49	89.1	108	2	PH0968	Ig kappa chain V-I
19	49	89.1	108	2	H44151	Ig kappa chain V-I
20	49	89.1	109	2	PH0963	Ig kappa chain V-I
21	49	89.1	109	2	B30601	Ig kappa chain V-I
22	49	89.1	109	2	A30608	Ig kappa chain V-I
23	49	89.1	109	2	D30601	Ig kappa chain V-I
24	49	89.1	109	2	F30607	Ig kappa chain V-I
25	49	89.1	109	2	C30601	Ig kappa chain V-I
26	49	89.1	109	2	H30601	Ig kappa chain V-I
27	49	89.1	116	2	B27594	Ig kappa chain V-I
28	49	89.1	121	2	S40327	Ig kappa chain V-I
29	49	89.1	129	1	K3H0M1	Ig kappa chain V-I

30	49	89.1	129	1	K3H0M1	Ig kappa chain pre
31	49	89.1	129	2	S46369	Ig light chain var
32	49	89.1	134	2	S38643	Ig kappa chain V-I
33	49	89.1	114	2	S46375	Ig kappa chain V-I
34	47	85.5	93	2	S37505	Ig kappa chain V-I
35	47	85.5	109	2	B30601	Ig kappa chain V-I
36	46	83.6	47	2	G30607	Ig kappa chain V-I
37	46	83.6	62	2	130601	Ig kappa chain V-I
38	46	83.6	92	2	S37510	Ig kappa chain V-I
39	46	83.6	96	2	S45441	Ig kappa chain V-I
40	46	83.6	109	1	K3H0M1	Ig kappa chain V-I
41	46	83.6	111	2	S40359	Ig kappa chain V-I
42	46	83.6	116	2	C27594	Ig kappa chain pre
43	46	83.6	116	2	S41817	Ig kappa chain V-I
44	46	83.6	119	2	S41816	Ig kappa chain V-I
45	45	81.8	87	2	S16843	Ig kappa chain V-I

ALIGNMENTS

RESULT 1
130607
Ig kappa chain V-I region (Wei) - human (fragments)
C/Species: Homo sapiens (man)
C/Date: 29-Jun-1985 #sequence_revision 29-Jun-1985 #text_change 09-May-1997
C/Accession: 130607
R/Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; S
J. Immunol. 142, 3158-3163, 1989
A/Title: Structural and idiotype characterization of the L chains of human IGM autoa
A/Reference number: A30601; MUID:89215279; PMID:2496160
A/Accession: 130607
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-83 <GON>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 89.1%; Score 49; DB 2; Length 83;
Best Local Similarity 91.7%; Pred. No. 0.0089;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
Db 24 RASQSVSSSYLA 35

RESULT 2

136823
Ig kappa chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
R/Blaisson, G.; Kuntz, J.L.; Paeguali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A/Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid ;
A/Reference number: S16823; MUID:91243737; PMID:1903706
A/Accession: S16823
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-87 <BLA>
A/Cross-references: EMBL:X54821
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/7-82/Domain: immunoglobulin homology <IRM>

Query Match 89.1%; Score 49; DB 2; Length 87;
Best Local Similarity 91.7%; Pred. No. 0.0094;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 RASQSVSSSYLA 12
Db 15 RASQSVSSSYLA 26

Db 61 ADYKGFITSRDNRKNTLYLQNMNLSRAEDTAIYCA-RDMDKCH-ALPDTMGCTLVTS 119

QY 117 S 117

Db 120 S 120

RESULT 2

US-08-331-398A-46
Sequence 46, Application US/08331398A
Patent No. 5608039
GENERAL INFORMATION:
APPLICANT: Paetan, Ira
APPLICANT: Willingham, Mark
APPLICANT: Fitzgerald, David
APPLICANT: Birkmann, Ulrich
APPLICANT: Pal, Lee
TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
TITLE OF INVENTION: and Their Uses (as amended)
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Plaza
City: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,398A
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note="Human fetal immunoglobulin
OTHER INFORMATION: 56P1/CL Variable Heavy chain (V-H)"
US-08-331-398A-46

Query Match

Best Local Similarity 86.7%; Score 549.5; DB 1; Length 119;
Matches 106; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVQLVDSGPGGVGPGSRRLSCAASGFTFSYTHMVRQAQKGLIEWTFISYDGNKNTY 60
Db 1 QVQLVDSGPGGVGPGSRRLSCAASGFTFSYTHMVRQAQKGLIEWTFISYDGNKNTY 60
QY 61 ADYKGFITSRDNRKNTLYLQNMNLSRAEDTAIYCA-RDMDKCH-ALPDTMGCTLVTS 118

Db 61 ADYKGFITSRDNRKNTLYLQNMNLSRAEDTAIYCA-RDMDKCH-ALPDTMGCTLVTS 119

RESULT 3

US-08-331-397B-46
Sequence 46, Application US/08331397B
Patent No. 5981726
GENERAL INFORMATION:
APPLICANT: Paetan, Ira
APPLICANT: Benhar, Itai
TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
Specific Antibody Fragments, Fusion Proteins, and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Plaza
City: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,397B
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126120US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note="Human fetal immunoglobulin
OTHER INFORMATION: 56P1/CL Variable Heavy chain (V-H)"
US-08-331-397B-46

Query Match

Best Local Similarity 86.7%; Score 549.5; DB 2; Length 119;
Matches 106; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVQLVDSGPGGVGPGSRRLSCAASGFTFSYTHMVRQAQKGLIEWTFISYDGNKNTY 60
Db 1 QVQLVDSGPGGVGPGSRRLSCAASGFTFSYTHMVRQAQKGLIEWTFISYDGNKNTY 60
QY 61 ADYKGFITSRDNRKNTLYLQNMNLSRAEDTAIYCA-RDMDKCH-ALPDTMGCTLVTS 118
Db 61 ADYKGFITSRDNRKNTLYLQNMNLSRAEDTAIYCA-RDMDKCH-ALPDTMGCTLVTS 119

RESULT 4

US-08-759-804A-46

GenCore version 5.1.4.P5.4578
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OM protein - protein search, using SW model

Run on: April 16, 2003, 17:15:40 ; Search time 30.2246 Seconds

(without alignments)
114,870 Million cell updates/sec

Title: US-09-644-668a-17

Sequence: 1 QVQLVSGGSGGVQPGRLRL.....TGMIGPDYWGQGLTVTVSS 118

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: Issued_Patents_AA:
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2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	558.5	88.1	120	1	US-07-942-245-35 Sequence 35, Appl
2	549.5	86.7	119	1	US-08-331-398A-46 Sequence 46, Appl
3	549.5	86.7	119	2	US-08-331-397B-46 Sequence 46, Appl
4	549.5	86.7	119	2	US-08-759-804A-46 Sequence 46, Appl
5	549.5	86.7	119	4	US-09-227-693-46 Sequence 46, Appl
6	533.5	84.1	117	4	US-09-025-769B-24 Sequence 24, Appl
7	530.5	83.7	116	1	US-08-211-202-141 Sequence 141, Appl
8	529.5	83.7	125	4	US-09-240-274-24 Sequence 24, Appl
9	529.5	83.5	125	4	US-09-240-274-9 Sequence 9, Appl
10	524.5	82.7	125	4	US-09-240-274-8 Sequence 8, Appl
11	524.5	82.7	125	4	US-09-240-274-20 Sequence 20, Appl
12	524.5	82.7	125	4	US-09-240-274-22 Sequence 22, Appl
13	524.5	82.7	125	4	US-09-240-274-149 Sequence 149, Appl
14	523.5	82.5	126	4	US-09-240-274-10 Sequence 10, Appl
15	520	82.0	128	4	US-09-240-274-1 Sequence 1, Appl
16	517	81.5	125	4	US-09-079-029-11 Sequence 11, Appl
17	516.5	81.5	125	4	US-09-240-274-33 Sequence 33, Appl
18	515	81.2	126	4	US-09-240-274-10 Sequence 10, Appl
19	515	81.2	126	4	US-09-240-274-144 Sequence 144, Appl
20	514.5	81.2	126	4	US-09-240-274-150 Sequence 150, Appl
21	514.5	81.1	128	4	US-09-240-274-6 Sequence 6, Appl
22	514	81.1	122	2	US-07-934-373C-21 Sequence 142, Appl
23	513	80.9	122	2	US-08-437-642B-21 Sequence 21, Appl
24	513	80.9	122	3	US-08-146-206C-21 Sequence 21, Appl
25	513	80.9	122	5	PCT-US93-07832-21 Sequence 21, Appl
26	513	80.9	122	5	US-09-240-274-152 Sequence 152, Appl
27	513	80.9	126	4	US-09-240-274-152 Sequence 152, Appl

28	509.5	80.4	117	4	US-09-157-370-1	Sequence 1, Appl
29	509	80.3	124	4	US-09-240-274-4	Sequence 4, Appl
30	508	80.1	120	4	US-09-025-769B-38	Sequence 38, Appl
31	508	80.1	120	4	US-09-025-769B-63	Sequence 63, Appl
32	508	80.1	141	1	US-08-259-372A-2	Sequence 2, Appl
33	508	80.1	141	1	US-08-468-671-2	Sequence 2, Appl
34	508	80.1	281	4	US-09-025-769B-118	Sequence 118, Appl
35	507.5	80.0	123	2	US-08-665-202-30	Sequence 30, Appl
36	507	80.0	123	4	US-08-983-607-38	Sequence 38, Appl
37	506	79.8	117	1	US-07-942-245-35	Sequence 35, Appl
38	504	79.5	131	4	US-08-983-607-28	Sequence 28, Appl
39	502.5	79.3	127	4	US-09-240-274-139	Sequence 139, Appl
40	502.5	79.3	129	4	US-09-240-274-143	Sequence 143, Appl
41	502	79.2	124	4	US-08-157-101A-7	Sequence 7, Appl
42	502	79.2	459	1	US-08-157-101A-7	Sequence 7, Appl
43	501.5	79.1	127	4	US-09-240-274-18	Sequence 18, Appl
44	501	79.0	125	1	US-08-276-852-76	Sequence 76, Appl
45	501	79.0	125	1	US-08-899-575-76	Sequence 76, Appl

ALIGNMENTS

RESULT 1
US-07-942-245-35
Sequence 35, Application US/07942245
Patent No. 5639641
GENERAL INFORMATION:
APPLICANT: PEDERSEN, Jan T.
APPLICANT: SEARLE, Stephen M.J.
APPLICANT: REES, Anthony R.
APPLICANT: ROGUSKA, Michael A.
APPLICANT: GUILD, Braydon C.
TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
NUMBER OF SEQUENCES: 522
CORRESPONDENCE ADDRESSES:
ADDRESS: Sughrie, Mion, Zimm, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
SOFTWARE: In house
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,245
FILING DATE: 09-SEP-1992
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-942-245-35
Query Match 88.1%; Score 558.5; DB 1; Length 120;
Best Local Similarity 89.3%; Pred. No. 8.3e-47;
Matches 108; Conservative 2; Mismatches 6; Indels 5; Gaps 2;
QY 1 QVQLVSGGSGGVQPGRLRLSCAASGFTSSYTHWTRQAPKGLVNTFTISYGNKKY 60
Db 1 QVQLVSGGSGGVQPGRLRLSCAASGFTSSYTHWTRQAPKGLVNTFTISYGNKKY 60
QY 61 ADSVKGRTISRDNSKNTLYLQNNLSLRAPDFAIYCAET-----GMLGPFQYWGQGLTVTV 116

Db 121 TVSS 124

RESULT 2

US-09-880-748-1519
Sequence 1519, Application US/09880748
Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1519

LENGTH: 252

TYPE: PRT

ORGANISM: Homo sapiens

US-09-880-748-1519

Query Match

Best Local Similarity 86.3%; Score 562; DB 9; Length 252;

Matches 107; Conservative 5; Mismatches 6; Indels 6; Gaps 1;

Db 121 TVSS 124

Query Match

Best Local Similarity 86.3%; Score 562; DB 9; Length 252;

Matches 107; Conservative 5; Mismatches 6; Indels 6; Gaps 1;

Db 121 TVSS 124

Query Match

Best Local Similarity 86.3%; Score 562; DB 9; Length 252;

Matches 107; Conservative 5; Mismatches 6; Indels 6; Gaps 1;

Db 121 TVSS 124

Query Match

Best Local Similarity 86.3%; Score 562; DB 9; Length 252;

Matches 107; Conservative 5; Mismatches 6; Indels 6; Gaps 1;

Db 121 TVSS 124

Query Match

Best Local Similarity 86.3%; Score 562; DB 9; Length 252;

Matches 107; Conservative 5; Mismatches 6; Indels 6; Gaps 1;

Db 121 TVSS 124

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Best Local Similarity 86.3%; Score 562; DB 9; Length 252;

ORGANISM: Homo sapiens

US-09-880-748-983

Query Match

Best Local Similarity 88.3%; Score 560; DB 9; Length 254;
Matches 108; Conservative 5; Mismatches 5; Indels 10; Gaps 2;

GENERAL INFORMATION:

APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1201

LENGTH: 252

TYPE: PRT

ORGANISM: Homo sapiens

US-09-880-748-1201

Query Match

Best Local Similarity 87.9%; Score 557; DB 9; Length 252;

Matches 106; Conservative 6; Mismatches 6; Indels 6; Gaps 1;

Db 121 TVSS 124

Query Match

Best Local Similarity 87.9%; Score 557; DB 9; Length 252;

Matches 106; Conservative 6; Mismatches 6; Indels 6; Gaps 1;

Db 121 TVSS 124

Query Match

Best Local Similarity 87.9%; Score 557; DB 9; Length 252;

Matches 106; Conservative 6; Mismatches 6; Indels 6; Gaps 1;

Db 121 TVSS 124

Query Match

Best Local Similarity 87.9%; Score 557; DB 9; Length 252;

Matches 106; Conservative 6; Mismatches 6; Indels 6; Gaps 1;

Db 121 TVSS 124

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Best Local Similarity 87.9%; Score 557; DB 9; Length 252;

Matches 106; Conservative 6; Mismatches 6; Indels 6; Gaps 1;

Db 121 TVSS 124

Query Match

Best Local Similarity 87.9%; Score 557; DB 9; Length 252;

GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2003, 17:21:54 ; Search time 34.7789 Seconds

(without alignments)
256.547 Million cell updates/sec

Title: US-09-644-668a-17

Sequence: 1 QVQLVSGGSGGVVQPGSRSLRL.....TGMLEPFDYWGCTLVTVSS 118

Scoring table: BLOSUM62

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Searched: 288829 seqs, 75613865 residues

TD: number of hits satisfying chosen parameters: 288829

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
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- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	562	88.6	252	9	US-09-880-748-1519
3	560	88.3	254	9	US-09-880-748-983
4	557	87.9	252	9	US-09-880-748-1201
5	550	86.8	252	9	US-09-880-748-1627
6	549	86.6	249	9	US-09-880-748-1109
7	546.5	86.2	248	9	US-09-880-748-1421
8	541.5	85.4	241	9	US-09-880-748-2055
9	541	85.3	253	9	US-09-880-748-1200
10	540	85.2	252	9	US-09-880-748-956
11	539	85.0	249	9	US-09-880-748-512
12	537	84.7	254	9	US-09-880-748-977
13	535.5	84.5	252	9	US-09-880-748-1731
14	534	84.2	254	9	US-09-880-748-881
15	532	83.9	244	9	US-09-880-748-1910
16	532	83.9	247	9	US-09-880-748-1330
17	530.5	83.7	125	9	US-09-848-798-24
18	529.5	83.5	125	9	US-09-848-798-9
19	529.5	83.5	240	9	US-09-880-748-1898

20	528	83.3	254	9	US-09-880-748-1759	Sequence 1759, Ap
21	527.5	83.2	252	9	US-09-880-748-988	Sequence 988, App
22	527.5	83.2	252	9	US-09-880-748-1394	Sequence 1394, Ap
23	526	83.0	251	9	US-09-880-748-952	Sequence 952, App
24	526	83.0	251	9	US-09-880-748-982	Sequence 982, App
25	526	83.0	251	9	US-09-880-748-1512	Sequence 1512, Ap
26	526	83.0	251	9	US-09-880-748-1554	Sequence 1554, Ap
27	525.5	82.9	251	9	US-09-880-748-955	Sequence 955, App
28	525	82.8	122	9	US-09-144-886-69	Sequence 69, App1
29	525	82.8	241	9	US-09-880-748-1887	Sequence 1887, Ap
30	525	82.8	241	9	US-09-880-748-1901	Sequence 1901, Ap
31	525	82.8	249	9	US-09-880-748-1890	Sequence 1890, Ap
32	525	82.8	249	9	US-09-880-748-1397	Sequence 1397, App
33	525	82.8	249	9	US-09-880-748-1102	Sequence 1102, Ap
34	525	82.8	249	9	US-09-880-748-1115	Sequence 1115, Ap
35	525	82.8	254	9	US-09-880-748-981	Sequence 981, App
36	524.5	82.7	125	9	US-09-848-798-8	Sequence 8, App1
37	524.5	82.7	125	9	US-09-848-798-20	Sequence 20, App1
38	524.5	82.7	125	9	US-09-848-798-21	Sequence 21, App1
39	524.5	82.7	125	9	US-09-848-798-22	Sequence 22, App1
40	524.5	82.7	249	9	US-09-880-748-912	Sequence 912, App
41	524	82.6	249	9	US-09-880-748-1724	Sequence 1724, Ap
42	524	82.6	249	9	US-09-880-748-1725	Sequence 1725, Ap
43	523	82.5	126	9	US-09-144-886-68	Sequence 68, App1
44	523	82.5	126	9	US-09-848-798-149	Sequence 149, App1
45	523	82.5	239	9	US-09-880-748-1882	Sequence 1882, Ap

ALIGNMENTS

RESULT 1
US-09-880-748-924
Sequence 924, Application US/09880748
Publication No. US2003005937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: P5523
CURRENT APPLICATION NUMBER: US/09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 924
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-924

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Best Local Similarity 88.7%; Pred. No. 8.6e-36;
Matches 110; Conservative 3; Mismatches 5; Indels 6; Gaps 1;

QY 1 QVQLVSGGSGGVVQPGSRSLRLSCAAGTFFSSYTMHWRAQPGKLEWVTFISYDGNKKY 60
DB 1 QVQLVSGGSGGVVQPGSRSLRLSCAAGTFFSSYTMHWRAQPGKLEWVAVISYDGNKKY 60
QY 61 ADSYKGFITSDRSKNTLTLQNNSLRAEDTAVYYCAR-----TGMLEPFDYWGCTLV 114
DB 61 ADSYKGFITSDRSKNTLTLQNNSLRAEDTAVYYCARPSDYILTYGLTYFDYWGCTLV 120
QY 115 TVSS 118
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GenCore version 5.1.4 p5.4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:56:17 ; Search time 93.5719 Seconds

(without alignments)
168.037 Million cell updates/sec

Title: US-09-644-668A-17

Perfect score: 634

Sequence: 1 QVQLVSGGSGVQPGSRSLRL.....TGMTPDYMCGQLTVTSS 118

Scoring table:

Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	634	100.0	118	22 AAB67508
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6	566.5	89.4	225	22 AAB93659
7	566.5	89.4	225	22 AAB9380
8	566.5	89.4	225	22 AAB75002
9	566.5	89.4	22	22 AAB75013
10	564	89.0	463	21 AAY93701

11	564	89.0	463	21 AAY93727	The heavy chain of
12	564	89.0	463	21 AAY93728	The heavy chain of
13	562	88.6	252	23 ABR45508	Human Blys binding
14	561.5	88.6	225	22 AAB9368	Human Interleukin
15	561.5	88.6	225	22 AAB75021	Anti-IL6 monoclonal
16	560.5	88.4	225	22 AAB9387	Human Interleukin
17	560.5	88.4	225	22 AAB95080	Anti-IL6 monoclonal
18	560	88.3	254	23 ABR44972	Human Blys binding
19	558.5	88.1	120	15 AAB52064	Heavy chain variab
20	558.5	88.1	225	22 AAB9367	Human Interleukin
21	558.5	88.1	225	22 AAB75000	Anti-IL6 monoclonal
22	558	88.0	463	21 AAY93707	The heavy chain of
23	557.5	87.9	463	21 AAY93732	The heavy chain of
24	557.5	87.9	119	22 AAB02515	Anti-adipocyte mon
25	557	87.9	252	23 ABR4510	Human Blys binding
26	555.5	87.6	519	23 AAB91933	Human secreted pro
27	554.5	87.5	225	22 AAB9389	Human Interleukin
28	554.5	87.5	225	22 AAB75022	Anti-IL6 monoclonal
29	554	87.4	118	23 ABR07230	Anti-IL-4 receptor
30	554	87.4	254	21 AAY56287	HCAT clone 25 ant
31	554	87.4	490	21 AAY56637	hCAT binding huma
32	552.5	87.1	225	22 AAB9361	Human Interleukin
33	552.5	87.1	225	22 AAB9385	Human Interleukin
34	552.5	87.1	225	22 AAB75014	Anti-IL6 monoclonal
35	552.5	87.1	225	22 AAB75018	Anti-IL6 monoclonal
36	551.5	87.0	115	21 AAB39519	Anti-IL12 antibody
37	550	86.8	252	23 ABR45616	Human Blys binding
38	549.5	86.7	119	17 ABR95216	Human foetal immu
39	549	86.6	249	23 ABR45098	Human anti-CD4 mo
40	549	86.6	119	22 ABR67516	Heavy chain variab
41	547.5	86.4	117	23 ABR77063	AC285 antibody he
42	547	86.3	128	23 ABR45410	Human Blys binding
43	546.5	86.2	122	22 ABR12883	Human anti-HER2/ne
44	546	86.1	222	22 AAY08598	Anti-human TNF- α
45	545	86.0	223	20	

ALIGNMENTS

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DT	29-MAY-2001 (first entry)
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XX	
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KW	cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;
KW	autoimmune disease; infectious disease; inflammation; allergy;
KW	rheumatoid arthritis; myasthenia gravis; lupus erythematosus;
KW	multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;
KW	transplant rejection; graft versus host disease.
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XX	
FH	Key
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PN	W0200114424-A2.
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XX	
PF	24-AUG-2000; 2000MO-US23356.

Location/Qualifiers
31..35
/note="CDR1"
50..66
/note="CDR2"
99..107
/note="CDR3"

QY 62 DSVKGRFTISRDNKNTLYLQNNSLRAEDTAIYCCARTGMGLPFDYWGGLTVTVSS 118
 DB 61 DSVKGRFTISRDNKNTLYLQNNSLRAEDTAIYCCARTGMGLPFDYWGGLTVTVSS 116

RESULT 2
 Q8WUK1
 ID 08WUK1 PRELIMINARY; PRT; 613 AA.
 AC 08WUK1
 DT 01-MAR-2002 (T-EMBLrel. 20, Created)
 DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
 DE Hypoetical 67.3 kDa protein.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RC ISSUE=TONSIL;
 RA Crausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC020240; AA020240.1; -
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR003597; IG_C1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG; 5.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IG_C1; 4.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
 DR Hypoetical protein.
 KM SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;

Query Match 85.6%; Score 543; DB 4; Length 613;
 Best local similarity 86.8%; Pred. No. 1.6e-46;
 Matches 105; Conservative 5; Mismatches 7; Indels 4; Gaps 2;

QY 1 QVQLVDSGGGVVQGRSLRLSCAASGFTSSYTMHWYRQAPGKLEWYTFISYDGNKYY 60
 DB 20 QVQLVDSGGGVVQGRSLRLSCAASGFTSSYTMHWYRQAPGKLEWYTFISYDGNKYY 79
 QY 61 ADSYKGRFTISRDNKNTLYLQNNSLRAEDTAIYCCARTGMGLPFDYWGGLTVTVSS 117
 DB 80 ADSYKGRFTISRDNKNTLYLQNNSLRAEDTAIYCCARTGMGLPFDYWGGLTVTVSS 138
 QY 118 S 118
 DB 139 S 139

RESULT 3
 Q9UL90
 ID 09UL90 PRELIMINARY; PRT; 113 AA.
 AC 09UL90
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region (fragment).
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; Pubmed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).

DR EMBL; AF035024; AAD56260.1; -
 DR HSP; P01772; 2F84.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IG; 1.
 FT NON_TER 1 1
 FT NON_TER 113 113
 SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 84.3%; Score 534.5; DB 4; Length 113;
 Best local similarity 86.4%; Pred. No. 1.5e-46;
 Matches 102; Conservative 5; Mismatches 6; Indels 5; Gaps 1;

QY 1 QVQLVDSGGGVVQGRSLRLSCAASGFTSSYTMHWYRQAPGKLEWYTFISYDGNKYY 60
 DB 1 QVQLVDSGGGVVQGRSLRLSCAASGFTSSYTMHWYRQAPGKLEWYTFISYDGNKYY 60
 QY 61 ADSYKGRFTISRDNKNTLYLQNNSLRAEDTAIYCCARTGMGLPFDYWGGLTVTVSS 118
 DB 61 ADSYKGRFTISRDNKNTLYLQNNSLRAEDTAIYCCARTGMGLPFDYWGGLTVTVSS 113

RESULT 4
 Q9Y509
 ID 09Y509 PRELIMINARY; PRT; 147 AA.
 AC 09Y509
 DT 01-NOV-1999 (T-EMBLrel. 12, Created)
 DT 01-NOV-1999 (T-EMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
 DE Vh3 protein (fragment).
 GN Vh3.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96071149; Pubmed=7475288;
 RA Cao J., Vesicic R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
 RA Lichtenstein A.K., Berenson J.R.;
 RT "A CD10-positive subset of malignant cells is identified in multiple
 RT myeloma using PCR with patient-specific immunoglobulin gene primers";
 RL Leukemia 9:1948-1953(1995).
 DR HSP; S80860; AAD14339.1; -
 DR HSP; P01772; 2F84.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IG; 1.
 FT NON_TER 1 1
 FT NON_TER 147 147
 SQ SEQUENCE 147 AA; 15768 MW; 8489FCAA7BC925C CRC64;

Query Match 78.4%; Score 497; DB 4; Length 147;
 Best local similarity 75.4%; Pred. No. 1.2e-42;
 Matches 95; Conservative 8; Mismatches 15; Indels 8; Gaps 1;

QY 1 QVQLVDSGGGVVQGRSLRLSCAASGFTSSYTMHWYRQAPGKLEWYTFISYDGNKYY 60
 DB 1 QVQLVDSGGGVVQGRSLRLSCAASGFTSSYTMHWYRQAPGKLEWYTFISYDGNKYY 60
 QY 61 ADSYKGRFTISRDNKNTLYLQNNSLRAEDTAIYCCARTGMGLPFDYWGGLTVTVSS 112
 DB 61 ADSYKGRFTISRDNKNTLYLQNNSLRAEDTAIYCCARTGMGLPFDYWGGLTVTVSS 120
 QY 113 LTVTVSS 118
 DB 121 LTVTVSS 126

RESULT 5
 Q9UL84
 ID 09UL84 PRELIMINARY; PRT; 122 AA.

GenCore version 5.1.4.P5.4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 17:13:59 ; Search time 120.898 seconds
(without alignments)
201.108 Million cell updates/sec

Title: US-09-644-668a-17

Sequence: 1 QVQVSGGGVQVQGRSLRL.....TGWLGPPDYWGQGLTVTVSS 118

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

To: number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Result No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	546.5	86.2	116	4	Q9UL93
2	543	85.6	613	4	Q8WTK1
3	534.5	84.3	113	4	Q9UL90
4	497	78.4	147	4	Q9Y509
5	496	78.2	122	4	Q9UL84
6	494.5	78.0	121	4	Q9UL71
7	482	76.0	118	4	Q9UL91
8	481.5	75.9	597	4	Q96BB9
9	478	75.4	573	4	Q8WU38
10	474	74.8	471	4	Q8WU38
11	469	74.0	118	4	Q8WU38
12	469	74.0	473	11	Q9UL72
13	458	72.2	112	4	Q9HCC1
14	449	70.8	494	4	Q96K68
15	438.5	69.2	119	11	Q920E7
16	438	69.1	487	11	Q99KX4

17	430.5	67.9	479	11	Q91WP5
18	423	66.7	95	4	Q9ULB6
19	412.5	65.1	131	4	Q9ULB8
20	405	63.9	469	11	Q8R3V9
21	400	63.1	298	11	Q9QYF0
22	394	62.1	484	11	Q8VEA0
23	392.5	61.9	104	4	Q9UL87
24	391.5	61.8	486	11	Q91Z07
25	386	60.9	124	4	Q9UL92
26	384.5	60.6	480	11	Q91XEL
27	382	60.3	437	11	Q9RI44
28	370.5	58.4	112	4	Q9UGP3
29	356.5	56.2	125	4	Q9UL95
30	354.5	55.9	484	11	Q99L66
31	352.5	55.6	119	4	Q9UL94
32	351	55.4	124	6	Q9N0W4
33	348	54.9	124	6	Q9N0W6
34	344.5	54.3	614	4	Q96GA6
35	344	54.3	241	11	Q921A6
36	343.5	54.2	142	11	Q924Q1
37	339.5	53.5	119	4	Q9UL73
38	338.5	53.4	473	11	Q9DBL4
39	335	52.8	145	11	Q924Q7
40	332	52.4	159	4	Q96C50
41	331.5	52.3	146	11	Q924Q8
42	331.5	52.3	481	11	Q91WT1
43	331	52.2	109	11	Q9UL75
44	330	52.1	121	11	Q99NG4
45	329.5	52.0	146	11	Q924R8

ALIGNMENTS

RESULT 1

Q9UL93 PRELIMINARY; PRT; 116 AA.
ID Q9UL93;
AC Q9UL93;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalle N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR HSSP; P01772; 2PB4.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGv_1.
FT NON_TER
FT TER
SQ SEQUENCE 116 AA; 12434 MW; ODA0348154DD6061 CRC64;

Query Match

Best Local Similarity 86.2%; Score 546.5; DB 4; Length 116;
Matches 106; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

QY 2 VQVSGGGVQVQGRSLRLSCASGFTFSSTYMHVQAPKGLBWTFTSYDGNKYYA 61
DB 1 VQVSGGGVQVQGRSLRLSCASGFTFSSTYMHVQAPKGLBWTFTSYDGNKYYA 60

DE Ig heavy chain V-III region GA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN NCBI_TaxId=9606;
 RP SEQUENCE
 RA MEDLINE=74175307; PubMed=4208843;
 RX Florent G., Lehman D., Putnam P.W.;
 RL "The switch point in mu heavy chains of human Igm immunoglobulins";
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
 MACROGLOBULIN.
 DR PIR; A02052; M3HUGA.
 DR HSSP; P01772; 2FB4.
 DR InterPro; IPR003006; Iq_MHC.
 DR InterPro; IPR003596; Iq_V.
 DR Pfam; PF00047; Iq; 1.
 DR SMART; SM00406; Iq; 1.
 DR Immunoglobulin V region.
 KW CD_RES 1
 FT NON_TER 122 122 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 122 AA; 13166 MW; 745B6959B84100A CRC64;
 Query Match 79.0%; Score 501; DB 1; Length 122;
 Best Local Similarity 73.0%; Pred. No. 3.6e-43;
 Matches 89; Conservative 22; Mismatches 7; Indels 4; Gaps 2;
 QY 1 QVQLVSGGAVVQPGKSLRLSCAASGFTSSYTMHWROAPKGLEMTVITSDGNNKYY 60
 DB 1 QVQLVSGGAVVQPGKSLRLSCAASGFTSSYTMHWROAPKGLEMTVITSDGNNKYY 60
 QY 61 ADSVKGRTISRDNSKNTLYLQMNLSLRADTAIYTCAR--TGMLEPPDYWGGLTVT 116
 DB 61 ADSVKGRTISRDNSKNTLYLQMNLSLRADTAIYTCAR--TGMLEPPDYWGGLTVT 120
 QY 117 SS 118
 DB 121 SS 122
 Db 121 SS 122
 RESULT 3
 HV31_HUMAN STANDARD; PRT; 119 AA.
 ID HV31_HUMAN
 AC P01770;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE "Ig heavy chain V-III region NIE."
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN NCBI_TaxId=9606;
 RP SEQUENCE
 RA MEDLINE=7070269; PubMed=826475;
 RX Ponetig1 H., Hilschmann N.;
 RL "The rule of antibody structure. The primary structure of a
 monoclonal IgG1 immunoglobulin (myeloma protein N1e). III. The
 chymotryptic peptides of the H-chain, alignment of the tryptic
 peptides and discussion of the complete structure."
 RL Hope-Sevler's Z. Physiol. Chem. 357:1571-1604(1976).
 CC DISULFIDE BOND.
 MEDLINE=7070267; PubMed=1002129;
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
 RL "Rule of antibody structure. The primary structure of a monoclonal
 IgG1 immunoglobulin (myeloma protein N1e). I: Purification and
 characterization of the protein, the L- and H-chains, the
 cyanogen bromide cleavage products, and the disulfide bridges."
 RL Hope-Sevler's Z. Physiol. Chem. 357:1515-1540(1976).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IG1 MYELOMA
 PROTEIN.

DR PIR; A02053; G1HUNI.
 DR HSSP; P01772; 2FB4.
 DR InterPro; IPR003006; Iq_MHC.
 DR InterPro; IPR003596; Iq_V.
 DR Pfam; PF00047; Iq; 1.
 DR SMART; SM00406; Iq; 1.
 DR Immunoglobulin V region.
 KW MOD_RES 1
 FT DISULFID 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT NON_TER 119 119
 SQ SEQUENCE 119 AA; 13242 MW; C96935A6B5E165B CRC64;
 Query Match 78.5%; Score 497.5; DB 1; Length 119;
 Best Local Similarity 75.6%; Pred. No. 7.7e-43;
 Matches 95; Conservative 11; Mismatches 10; Indels 5; Gaps 2;
 QY 1 QVQLVSGGAVVQPGKSLRLSCAASGFTSSYTMHWROAPKGLEMTVITSDGNNKYY 60
 DB 1 QVQLVSGGAVVQPGKSLRLSCAASGFTSSYTMHWROAPKGLEMTVITSDGNNKYY 60
 QY 61 ADSVKGRTISRDNSKNTLYLQMNLSLRADTAIYTCAR--TGMLEPPDYWGGLTVT 117
 DB 61 ADSVKGRTISRDNSKNTLYLQMNLSLRADTAIYTCAR--TGMLEPPDYWGGLTVT 118
 QY 118 S 118
 DB 119 S 119
 Db 119 S 119
 RESULT 4
 HV31_HUMAN STANDARD; PRT; 121 AA.
 ID HV31_HUMAN
 AC P01771;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE "Ig heavy chain V-III region HIL."
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN NCBI_TaxId=9606;
 RP SEQUENCE
 RA MEDLINE=79124695; PubMed=420800;
 RX Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
 RL "Amino acid sequence of the VH region of human myeloma
 cryoimmunoglobulin IgG H11."
 RL Biochemistry 18:553-560(1979).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IG1 MYELOMA
 PROTEIN.
 DR PIR; A02054; G1HHL.
 DR HSSP; P01772; 2FB4.
 DR InterPro; IPR003006; Iq_MHC.
 DR InterPro; IPR003596; Iq_V.
 DR Pfam; PF00047; Iq; 1.
 DR SMART; SM00406; Iq; 1.
 DR Immunoglobulin V region.
 KW MOD_RES 1
 FT NON_TER 121 121 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 121 AA; 13566 MW; 480FC53610EF5DAB CRC64;
 Query Match 76.7%; Score 486.5; DB 1; Length 121;
 Best Local Similarity 75.6%; Pred. No. 9.8e-42;
 Matches 93; Conservative 10; Mismatches 13; Indels 7; Gaps 2;
 QY 1 QVQLVSGGAVVQPGKSLRLSCAASGFTSSYTMHWROAPKGLEMTVITSDGNNKYY 60
 DB 1 QVQLVSGGAVVQPGKSLRLSCAASGFTSSYTMHWROAPKGLEMTVITSDGNNKYY 60
 QY 61 ADSVKGRTISRDNSKNTLYLQMNLSLRADTAIYTCAR--TGMLEPPDYWGGLTVT 115
 DB 61 GDSVKGRTISRDNSKNTLYLQMNLSLRADTAIYTCAR--TGMLEPPDYWGGLTVT 118

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:57:42 ; Search time 23.186 Seconds
(without alignments)
211.085 Million cell updates/sec

Title: US-09-644-668a-17
Perfect score: 63.4
Sequence: 1 QVALVESGGGVQPGSRRLT.....TGMIGPFDVGGGLVTYSS 118

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	526	83.0	122	1 HV3G_HUMAN	P01768 homo sapien
2	501	79.0	122	1 HV3H_HUMAN	P01769 homo sapien
3	497.5	78.5	119	1 HV3I_HUMAN	P01770 homo sapien
4	486.5	76.7	121	1 HV3J_HUMAN	P01771 homo sapien
5	480	75.7	126	1 HV3K_HUMAN	P01772 homo sapien
6	461	72.7	114	1 HV3B_HUMAN	P01763 homo sapien
7	460	72.6	116	1 HV3T_HUMAN	P01773 homo sapien
8	452.5	71.4	119	1 HV3L_HUMAN	P01781 homo sapien
9	450	71.0	136	1 HV3U_HUMAN	P01783 homo sapien
10	435	68.6	117	1 HV3C_HUMAN	P01782 homo sapien
11	432	68.1	119	1 HV3M_HUMAN	P01774 homo sapien
12	431.5	66.1	120	1 HV3E_HUMAN	P01766 homo sapien
13	430	67.8	119	1 HV3N_HUMAN	P01765 homo sapien
14	424	66.9	122	1 HV3A_HUMAN	P01762 homo sapien
15	423.5	66.8	115	1 HV3D_HUMAN	P01765 homo sapien
16	421	66.4	119	1 HV38_HUMAN	P01808 mus musculu
17	419.5	66.2	115	1 HV3F_HUMAN	P01767 homo sapien
18	417.5	65.9	116	1 HV05_CANF	P01811 carassius a
19	414	65.3	114	1 HV01_CANF	P01784 canis fami
20	413.5	65.2	115	1 HV32_MOUSE	P01801 mus musculu
21	413	65.1	119	1 HV37_MOUSE	P01807 mus musculu
22	412.5	65.1	142	1 HV01_RAT	P01805 mus musculu
23	411	64.8	117	1 HV30_HUMAN	P01776 homo sapien
24	408.5	64.0	113	1 HV30_MOUSE	P01799 mus musculu
25	406	64.0	119	1 HV40_MOUSE	P01810 mus musculu
26	405.5	63.6	113	1 HV27_MOUSE	P01796 mus musculu
27	403.5	63.5	113	1 HV39_MOUSE	P01809 mus musculu
28	402.5	63.2	113	1 HV31_MOUSE	P01802 mus musculu
29	400.5	63.0	115	1 HV33_MOUSE	P01802 mus musculu
30	398.5	62.8	117	1 HV54_MOUSE	P18525 mus musculu
31	398	62.7	113	1 HV28_MOUSE	P01797 mus musculu
32	397.5	62.7	113	1 HV28_MOUSE	P01797 mus musculu

34	397	62.6	111	1 HV35_MOUSE	P01804 mus musculu
35	396.5	62.5	113	1 HV34_MOUSE	P01803 mus musculu
36	396	62.5	112	1 HV20_MOUSE	P01789 mus musculu
37	393.5	62.1	113	1 HV29_MOUSE	P01798 mus musculu
38	393.5	62.1	116	1 HV3Q_HUMAN	P01778 homo sapien
39	393.5	62.1	117	1 HV17_MOUSE	P01786 mus musculu
40	392.5	61.9	117	1 HV41_MOUSE	P01811 mus musculu
41	392	61.8	117	1 HV55_MOUSE	P18526 mus musculu
42	390.5	61.6	123	1 HV25_MOUSE	P01794 mus musculu
43	390	61.5	118	1 HV3V_HUMAN	P80419 homo sapien
44	389.5	61.4	123	1 HV3P_MOUSE	P01793 mus musculu
45	389	61.4	119	1 HV3P_HUMAN	P01777 homo sapien

ALIGNMENTS

RESULT 1
HV3G_HUMAN

ID HV3G_HUMAN STANDARD; PRT; 122 AA.

AC P01768;
21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig heavy chain V-117 region CAM.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

RX MEDLINE=81013859; PubMed=6774332;
RA Lehman D.W., Putnam F.W.;

RT "Amino acid sequence of the variable region of a human mu chain:
location of a possible JH segment."

CC "MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
PATIENT WITH MACROGLOBULINEMIA.

DR HSSP; P01772; 2PB4.
DR InterPro; IPR003006; IG_MHC.

DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.

KW SMART; SM00406; IGV; 1.
FT MOD_RES 1
FT NON_TER 122

SEQUENCE 122 AA; 13668 MW; A42D0F17D252FIC2 CRC64;
PYRROLIDONE CARBOXYLIC ACID.

Query Match 83.0%; Score 526; DB 1; Length 122;
Best Local Similarity 79.5%; Pred. No. 1.2e-45;

Matches 97; Conservative 12; Mismatches 9; Indels 4; Gaps 1;

QY 1 QVALVESGGGVQPGSRRLTCAASGFTFSYTHWVQADGKLEWTFISYDGNKRY 60
1 QVELVESGGGVVZPGRSLRLSCAASGFTFSYTHWVQADGKLEWTFISYDGNKRY 60

DB 1 QVELVESGGGVVZPGRSLRLSCAASGFTFSYTHWVQADGKLEWTFISYDGNKRY 60
61 ADVYGRFTIRSDSKBTLTQNNLSLRRAEDTAIYYCART----GMIGPFDVGGGLVTY 116

DB 61 ADVYGRFTIRSDSKBTLTQNNLSLRRAEDTAIYYCART----GMIGPFDVGGGLVTY 116
117 SS 118

QY 117 SS 118
121 SS 122

DB 121 SS 122

RESULT 2
HV3H_HUMAN

ID HV3H_HUMAN STANDARD; PRT; 122 AA.
AC P01769;
21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig heavy chain V-117 region CAM.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

RX MEDLINE=81013859; PubMed=6774332;
RA Lehman D.W., Putnam F.W.;

A/Cross-references: GDB:118731, OMIM:146910
 A/Map position: 14q32.33-14q32.33
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 88.7%; Score 562.5; DB 2; Length 121;
 Best Local Similarity 89.3%; Pred. No. 2,3e-43;
 Matches 109; Conservative 2; Mismatches 6; Indels 5; Gaps 2;

Db 1 QVQLVESGGGVVQPGSRSLRSCAASGFTFSSTYTMHWROAPGKGLEWVTFISYDGNKKY 60
 1 QVQLVESGGGVVQPGSRSLRSCAASGFTFSSTYTMHWROAPGKGLEWVAIVISYDGNKKY 60

Qy 61 ADVKGRFTISRDNKNTLYIQMNSLRADTAIYCCARTG---GWLGPFDYWGQGLTVTV 116
 61 ADVKGRFTISRDNKNTLYIQMNSLRADTAIYCCARTGKRWKMGW-ALFDYWGQGLTVTV 119

Qy 117 SS 118
 120 SS 121

RESULT 3
 Ig heavy chain V region - human
 C/Species: Homo sapiens (man)
 C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C/Accession: S31598
 R/Cuisinier, A.M.; Gauthier, L.; Boudli, L.; Fougereau, M.; Tonnelie, C.
 Submitted to the EMBL Data Library, June 1992
 A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
 A/Reference number: S31585
 A/Accession: S31598
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-135 <CUI>
 A/Cross-references: EMBL:214170; NID:G31001; PIDN:CAA78539.1; PID:G31002
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F:31-114/Domain: immunoglobulin homology <IMM>

Query Match 88.4%; Score 560.5; DB 2; Length 135;
 Best Local Similarity 89.1%; Pred. No. 3,8e-43;
 Matches 106; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

Qy 1 QVQLVESGGGVVQPGSRSLRSCAASGFTFSSTYTMHWROAPGKGLEWVTFISYDGNKKY 60
 17 QVQLVESGGGVVQPGSRSLRSCAASGFTFSSTYTMHWROAPGKGLEWVAIFRYDGNKKY 76

Qy 61 ADVKGRFTISRDNKNTLYIQMNSLRADTAIYCCARTGWLGPFDYWGQGLTVTVSS 118
 77 ADVKGRFTISRDNKNTLYIQMNSLRADTAIYCCARTGWLGPFDYWGQGLTVTVSS 135

RESULT 4
 Ig heavy chain - human
 C/Species: Homo sapiens (man)
 C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
 C/Accession: S31116
 R/Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
 Eur. J. Immunol. 22, 247-251, 1992
 A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
 A/Reference number: S31104; MUID:92111633; PMID:11730252
 A/Accession: S31116
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-118 <RAA>
 A/Cross-references: EMBL:X62966
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.4%; Score 554; DB 2; Length 118;
 Best Local Similarity 89.0%; Pred. No. 1,3e-42;
 Matches 105; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy 1 QVQLVESGGGVVQPGSRSLRSCAASGFTFSSTYTMHWROAPGKGLEWVTFISYDGNKKY 60
 1 QVQLVESGGGVVQPGSRSLRSCAASGFTFSSTYTMHWROAPGKGLEWVAIVISYDGNKKY 60

Db 61 ADVKGRFTISRDNKNTLYIQMNSLRADTAIYCCARTGWLGPFDYWGQGLTVTVSS 118
 61 ADVKGRFTISRDNKNTLYIQMNSLRADTAIYCCARTGKRWKMGW-ALFDYWGQGLTVTVSS 118

Qy 117 SS 118
 120 SS 121

RESULT 5
 Ig heavy chain V region - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C/Accession: S31701
 R/Cuisinier, A.M.; Gauthier, L.; Boudli, L.; Fougereau, M.; Tonnelie, C.
 Submitted to the EMBL Data Library, June 1992
 A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
 A/Reference number: S31585
 A/Accession: S31701
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-137 <CUI>
 A/Cross-references: EMBL:214177; NID:G31020; PIDN:CAA78546.1; PID:G31021
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 87.2%; Score 553; DB 2; Length 137;
 Best Local Similarity 87.3%; Pred. No. 1,8e-42;
 Matches 103; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy 1 QVQLVESGGGVVQPGSRSLRSCAASGFTFSSTYTMHWROAPGKGLEWVTFISYDGNKKY 60
 20 QVQLVESGGGVVQPGSRSLRSCAASGFTFSSTYTMHWROAPGKGLEWVAIVISYDGNKKY 79

Qy 61 ADVKGRFTISRDNKNTLYIQMNSLRADTAIYCCARTGWLGPFDYWGQGLTVTVSS 118
 Db 80 PDVKGKFTISRDNKNTLYIQMNSLRADTAIYCCARTGWLGPFDYWGQGLTVTVSS 137

RESULT 6
 Ig heavy chain - human
 C/Species: Homo sapiens (man)
 C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
 C/Accession: S31117
 R/Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
 Eur. J. Immunol. 22, 247-251, 1992
 A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
 A/Reference number: S31104; MUID:92111633; PMID:11730252
 A/Accession: S31117
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-122 <RAA>
 A/Cross-references: EMBL:X62967
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.1%; Score 552; DB 2; Length 122;
 Best Local Similarity 87.7%; Pred. No. 2e-42;
 Matches 107; Conservative 3; Mismatches 8; Indels 4; Gaps 1;

Qy 1 QVQLVESGGGVVQPGSRSLRSCAASGFTFSSTYTMHWROAPGKGLEWVTFISYDGNKKY 60
 1 QVQLVESGGGVVQPGSRSLRSCAASGFTFSSTYTMHWROAPGKGLEWVAIVISYDGNKKY 60

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 17:11:36 / Search time 36.4351 Seconds

(without alignments)
311.344 Million cell updates/sec

Title: US-09-644-668a-17

Perfect score: 634

Sequence: 1 QVQLVSGGSGGVQPGRSRLT.....TCWLGPFDYWGQGLTVTVSS 118

Scoring table: BLOSUM62

Gapop 10.0 / Gapext 0.5

Searched: 283224 seqs, 96134422 residues

To: Number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

1: PIR 73:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	566.5	89.4	121	S19666	Ig heavy chain V r
2	562.5	88.7	121	G36005	Ig heavy chain V r
3	560.5	88.4	135	S31598	Ig heavy chain V r
4	554	87.4	118	S31116	Ig heavy chain - h
5	553	87.2	137	S31701	Ig heavy chain V r
6	552	87.1	122	S31117	Ig heavy chain - h
7	551	86.9	140	S70442	Ig heavy chain pre
8	548.5	86.5	134	S31679	Ig heavy chain V r
9	548	86.4	114	S46390	Ig heavy chain V r
10	547	86.3	122	E36005	Ig heavy chain V r
11	545	86.0	120	S31112	Ig heavy chain V r
12	544.5	85.9	132	S31603	Ig heavy chain - h
13	543.5	85.7	119	F36005	Ig heavy chain V r
14	541.5	85.4	133	A49028	Ig heavy chain V-I
15	541	85.3	139	S31674	Ig heavy chain V r
16	540.5	85.3	130	S31601	Ig heavy chain V r
17	527	83.1	114	S46392	Ig heavy chain V r
18	526.5	83.0	130	P10098	Ig heavy chain V r
19	526	83.0	122	M3H0M	Ig heavy chain pre
20	525	82.8	128	S48797	Ig heavy chain V-I
21	524.5	82.7	109	P16466	Ig heavy chain V r
22	524	82.6	133	S31510	Ig heavy chain V r
23	522	82.3	151	A60943	Ig heavy chain - h
24	520.5	82.1	123	S38493	Ig heavy chain pre
25	517	81.5	114	S46391	Ig heavy chain - h
26	516.5	81.5	119	C36005	Ig heavy chain V r
27	515.5	81.3	109	P16444	Ig heavy chain V r
28	510	80.4	120	S44111	Ig heavy chain V-D
29	509.5	80.4	111	P16445	Ig heavy chain V r

30	509	80.3	122	2	S69910	Ig V-D-J region (K
31	508.5	80.2	111	2	P16443	Ig heavy chain V r
32	508.5	80.2	119	2	S31108	Ig heavy chain - h
33	507.5	80.0	143	2	S23624	Ig heavy chain V r
34	506.5	79.9	123	2	S31114	Ig heavy chain - h
35	506	79.8	120	2	S48798	Ig heavy chain V r
36	505	79.7	118	2	S31677	Ig heavy chain V r
37	504.5	79.6	117	2	S78486	Ig heavy chain V r
38	503.5	79.4	140	2	S31686	Ig heavy chain V r
39	502.5	79.3	119	2	S31107	Ig heavy chain V r
40	501	79.0	122	1	M3H0M	Ig heavy chain - h
41	501	79.0	106	2	S31587	Ig heavy chain V-I
42	499	78.7	138	2	P16442	Ig heavy chain V r
43	498.5	78.6	113	2	S38490	Ig heavy chain - h
44	498.5	78.6	119	2	D36005	Ig heavy chain V r
45	498	78.5	124	2	S20782	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S19666
Ig heavy chain V region (VH3D4) - human

C/Species: Homo sapiens (man)
C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000

C/Accession: S19666

R/Marks: J D.; Hoogenboom, H.R.; Bonnett, T.P.; McCafferty, J.; Griffiths, A.D.; Wint

J. Mol. Biol. 222, 581-597, 1991

A/Title: By-passing immunization. Human antibodies from V-gene libraries displayed on

A/Reference number: S19663; MUID:92085276; PMID:1748994

A/Accession: S19666

A/Molecule type: mRNA

A/Residues: 1-121 <MAN>

A/Cross-references: EMBL:X61646; NID:G37688; PIN:CAA43827.1; PID:91335369

C/Superfamily: Immunoglobulin V region; Immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F15-98/Domain: Immunoglobulin homology <IMM>

Query Match

Best local similarity 89.4%; Score 566.5; DB 2; Length 121;
Matches 108; Conservative 5; Mismatches 5; Indels 3; Gaps 1;

Qy	1	QVQLVSGGSGGVQPGRSRLTSCASGFTSSYTHMWRQAPGKLEWTFISYDGNKXY 60
Db	1	QVQLVSGGSGGVQPGRSRLTSCASGFTSSYTHMWRQAPGKLEWTFISYDGNKXY 60
Qy	61	ADSVKGRFTISRDNSKNTLYQNMSLRADDTAIYCAETGW---LGPDYWGQGLTVTVS 117
Db	61	ADSVKGRFTISRDNSKNTLYQNMSLRADDTAIYCAETGW---LGPDYWGQGLTVTVS 120
Qy	118	S 118
Db	121	S 121

RESULT 2

G36005
Ig heavy chain V region (VH4) - human

C/Species: Homo sapiens (man)
C/Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998

C/Accession: G36005

R/Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990

A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable ge

A/Reference number: A36005; MUID:90349571; PMID:2117273

A/Accession: G36005

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-121 <SCH>

A/Cross-references: GB:M34031

C/Genetics:

A/Gene: GDB:IGH@; IGHV1

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAHWYQKPGAPRLIYGAFSRATGIP 60
1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAHWYQKPGAPRLIYGAFSRATGIP 60
Db 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAHWYQKPGAPRLIYGAFSRATGIP 60
QY 61 DRFGSGSGTDFTLTISRLEPEDPAVYVCCQYGSSPMTFGGTVEIK 108
61 DRFGSGSGTDFTLTISRLEPEDPAVYVCCQYGSSPMTFGGTVEIK 108
Db 61 DRFGSGSGTDFTLTISRLEPEDPAVYVCCQYGSSPMTFGGTVEIK 108

RESULT 2
US-09-240-274-178
Sequence 178, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
PTE REFERENCE: 09596-4202
ENT FILING DATE: 1999-01-29
ENT APPLICATION NUMBER: US/09/240,274
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 178
LENGTH: 108
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH52
US-09-240-274-178

Query Match 95.1%; Score 538; DB 4; Length 108;
Best Local Similarity 97.1%; Pred. No. 1.8e-42;
Matches 102; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 LITQSPGTLISLSPGERATLSCRASQSVSSSYLAHWYQKPGAPRLIYGAFSRATGIP 63
3 LITQSPGTLISLSPGERATLSCRASQSVSSSYLAHWYQKPGAPRLIYGAFSRATGIP 63
Db 3 LITQSPGTLISLSPGERATLSCRASQSVSSSYLAHWYQKPGAPRLIYGAFSRATGIP 63

QY 64 SGGSGGTDFLTISRLEPEDPAVYVCCQYGSSPMTFGGTVEIK 108
64 SGGSGGTDFLTISRLEPEDPAVYVCCQYGSSPMTFGGTVEIK 108
Db 64 SGGSGGTDFLTISRLEPEDPAVYVCCQYGSSPMTFGGTVEIK 108

US-09-232-081B-42
Sequence 42, Application US/08232081B
Patent No. 5886152
GENERAL INFORMATION:
APPLICANT: NAKATANI, TOMOYUKI
APPLICANT: GOMI, HIDEYUKI
APPLICANT: WIDENES, JOHN
APPLICANT: NOGUCHI, HIROSHI
TITLE OF INVENTION: HUMANIZED B-B10
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,081B

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAHWYQKPGAPRLIYGAFSRATGIP 60
1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAHWYQKPGAPRLIYGAFSRATGIP 60
Db 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAHWYQKPGAPRLIYGAFSRATGIP 60
QY 61 DRFGSGSGTDFTLTISRLEPEDPAVYVCCQYGSSPMTFGGTVEIK 108
61 DRFGSGSGTDFTLTISRLEPEDPAVYVCCQYGSSPMTFGGTVEIK 108
Db 61 DRFGSGSGTDFTLTISRLEPEDPAVYVCCQYGSSPMTFGGTVEIK 108

RESULT 4
US-08-488-113B-150
Sequence 150, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAHWYQKPGAPRLIYGAFSRATGIP 60
1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAHWYQKPGAPRLIYGAFSRATGIP 60
Db 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAHWYQKPGAPRLIYGAFSRATGIP 60
QY 61 DRFGSGSGTDFTLTISRLEPEDPAVYVCCQYGSSPMTFGGTVEIK 108
61 DRFGSGSGTDFTLTISRLEPEDPAVYVCCQYGSSPMTFGGTVEIK 108
Db 61 DRFGSGSGTDFTLTISRLEPEDPAVYVCCQYGSSPMTFGGTVEIK 108

Query Match 94.7%; Score 536; DB 2; Length 108;
Best Local Similarity 96.3%; Pred. No. 2.7e-42;
Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

US-08-232-081B-42
FILING DATE: 424
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20-3484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-232-081B-42

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using SW model

Run on: April 16, 2003, 17:15:40 ; Search time 27.6632 Seconds
(without alignments)
114.870 Million cell updates/sec

Title: US-09-644-668a-7

Perfect score: 566
Sequence: 1 EIVTQSPGTLISLPGERAT.....COQYGSPPWFGGCTKVEIK 108

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Top number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

1: Issued Patents AA.*
2: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backtile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	540	95.4	109	4	US-09-025-769B-16
2	538	95.1	108	4	US-09-240-274-178
3	536	94.7	108	2	US-08-232-081B-42
4	532	94.0	108	1	US-08-488-113B-150
5	532	94.0	108	1	US-08-477-484B-150
6	532	94.0	108	2	US-08-646-360-150
7	532	94.0	108	4	US-08-839-765-150
8	532	94.0	108	4	US-09-136-389-150
9	532	94.0	108	4	US-09-610-838-150
10	515.5	91.1	107	1	US-08-107-669D-14
11	515.5	91.1	107	1	US-08-472-788A-14
12	515.5	91.1	107	2	US-08-477-531B-14
13	515.5	91.1	107	2	US-08-082-842A-14
14	515	91.0	108	1	US-07-634-278-86
15	515	91.0	108	1	US-08-477-728-86
16	515	91.0	108	1	US-08-474-040-86
17	515	91.0	108	4	US-08-487-200-86
18	515	91.0	108	4	US-08-484-537-86
19	513	90.6	108	1	US-08-276-852-86
20	513	90.6	108	1	US-08-899-575-86
21	513	90.6	108	1	US-08-899-575-86
22	513	90.6	108	5	PCT-US95-08743-86
23	511	90.3	150	4	US-08-862-124-5
24	511	90.3	287	4	US-08-862-124-17
25	510.5	90.2	304	4	US-08-862-124-14
26	510.5	90.2	107	2	US-08-652-558-49
27	502	88.7	108	1	US-08-276-852-99

28	502	88.7	108	1	US-08-899-575-99	Sequence 99, Appl
29	502	88.7	108	1	US-08-899-575-99	Sequence 99, Appl
30	502	88.7	108	5	PCT-US95-08743-99	Sequence 99, Appl
31	501	88.5	129	2	US-08-480-774A-4	Sequence 4, Appl
32	493	87.1	110	4	US-09-025-769B-30	Sequence 30, Appl
33	493	87.1	110	4	US-09-025-769B-47	Sequence 47, Appl
34	492.5	87.0	134	4	US-08-405-034-4	Sequence 4, Appl
35	491	86.7	109	1	US-08-162-102C-23	Sequence 23, Appl
36	491	86.7	109	5	PCT-US93-08786-23	Sequence 147, App
37	489.5	86.5	109	1	US-08-276-852-147	Sequence 147, App
38	489.5	86.5	109	1	US-08-899-575-147	Sequence 147, App
39	489.5	86.5	109	1	US-08-899-575-147	Sequence 147, App
40	489.5	86.5	109	5	PCT-US95-08743-147	Sequence 147, App
41	487	86.0	104	1	US-08-276-852-100	Sequence 100, App
42	487	86.0	104	1	US-08-899-575-100	Sequence 100, App
43	487	86.0	104	1	US-08-899-575-100	Sequence 100, App
44	487	86.0	104	5	PCT-US95-08743-100	Sequence 100, App
45	487	86.0	107	1	US-08-276-852-90	Sequence 90, Appl

ALIGNMENTS

RESULT 1
US-09-025-769B-16
Sequence 16, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthum, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-16
Query Match 95.4%; Score 540; DB 4; Length 109;
Best Local Similarity 96.3%; Pred. No. 1.2e-42;
Matches 104; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that immunospecifically bind Blys
FILE REFERENCE: P5523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ. ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1499
LENGTH: 253
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1499

Query Match 91.3%; Score 517; DB 9; Length 253;
Best Local Similarity 93.5%; Pred. No. 8,4e-30;
Matches 101; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQKQKQAPRLIYGAFSRATGIP 60
DB 145 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQKQKQAPRLIYGASRRATGIP 204

QY 61 DRFGSGSGTDFLTISRLEPEDFAVYCCQYSSPMTFGQTKVEIK 108
DB 205 DRFGSGSGTDFLTISRLEPEDFAVYCCQYSSPMTFGQTKVEIK 252

RESULT 3
US-09-880-748-1264
Sequence 1264, Application US/09880748
Publication No. US2003005937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that immunospecifically bind Blys
FILE REFERENCE: P5523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
OR APPLICATION NUMBER: 60/212,210
OR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ. ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1264
LENGTH: 246
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1264

Query Match 90.9%; Score 514.5; DB 9; Length 246;
Best Local Similarity 95.4%; Pred. No. 1.2e-29;
Matches 103; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQKQKQAPRLIYGAFSRATGIP 60
DB 139 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQKQKQAPRLIYGASRRATGIP 198

QY 61 DRFGSGSGTDFLTISRLEPEDFAVYCCQYSSPMTFGQTKVEIK 108
DB 199 DRFGSGSGTDFLTISRLEPEDFAVYCCQYSS-LTRFGGTKVEIK 245

RESULT 4
US-08-844-215-8
Sequence 8, Application US/08844215
Patent No. US20020016445A1
GENERAL INFORMATION:
APPLICANT: PERSON, MATS AXEL
APPLICANT: ALANDER, TOBIAS ERIK
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,215
FILING DATE: 17-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/635,109
FILING DATE: 19-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 80146.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 325-7812
TELEFAX: (650) 325-7823
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-844-215-8

Query Match 90.8%; Score 514; DB 8; Length 107;
Best Local Similarity 93.3%; Pred. No. 6.8e-30;
Matches 98; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 LTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKQKQAPRLIYGAFSRATGIPDRF 63
DB 3 LTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKQKQAPRLIYGASRRATGIPDRF 62

QY 64 SGSGSGTDFLTISRLEPEDFAVYCCQYSSPMTFGQTKVEIK 108
DB 63 SGSGSGTDFLTISRLEPEDFAVYCCQYSSPMTFGQTKVEIK 107

RESULT 5
US-09-782-397-5
Sequence 5, Application US/09782397
Publication No. US20030021779A1
GENERAL INFORMATION:
APPLICANT: Dan, Michael D.
APPLICANT: Maltz, Pradip K.
APPLICANT: Kaplan, Howard A.
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING

Wed, Apr 16 17:35:28 2003

us-09-644-668a-7.rapb

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OM protein - protein search, using sw model

Run on: April 16, 2003, 17:21:54 ; Search time 31.8316 Seconds
(without alignments)
256.547 Million cell updates/sec

Title: US-09-644-668a-7
Sequence: 1 EIVLTQSPGTLISLSPGERAT.....CQYSSGPTFGQTKVEIK 108

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 288829 seqs, 75613885 residues

Total number of hits satisfying chosen parameters: 288829

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing filter 45 summaries

Database:

Published Applications AA:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep.*
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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
4: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB pep.*
7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB pep.*
9: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	538	95.1	108	9	US-09-848-798-178
2	517	91.3	253	9	US-09-880-748-1499
3	514.5	90.9	246	9	US-09-880-748-1264
4	514	90.8	107	8	US-08-844-215-8
5	511	90.3	150	9	US-09-782-397-5
6	511	90.3	287	9	US-09-782-397-17
7	511	90.3	304	9	US-09-782-397-14
8	508	89.8	108	9	US-09-300-425B-21
9	507	89.5	105	10	US-09-828-708-3
10	506.5	89.5	251	9	US-09-880-748-1219
11	506	89.4	107	8	US-08-844-215-10
12	505.5	89.3	236	10	US-09-859-053-34
13	503	88.9	105	10	US-09-828-708-7
14	503	88.9	110	9	US-10-001-934-40
15	500.5	88.4	212	9	US-10-006-553-118
16	497.5	87.9	236	10	US-09-859-053-38
17	493.5	87.2	252	9	US-09-880-748-1534
18	493	87.1	109	9	US-10-125-687-10
19	493	87.1	109	12	US-10-025-687-10

20	493	87.1	249	9	US-09-880-748-1035	Sequence 1035, Ap
21	487.5	86.1	245	9	US-09-880-748-1896	Sequence 1896, Ap
22	485.5	85.8	106	8	US-08-844-215-14	Sequence 14, Appl
23	485	85.7	96	9	US-10-194-975-82	Sequence 82, Appl
24	485	85.7	107	8	US-08-844-215-12	Sequence 12, Appl
25	484.5	85.6	254	9	US-09-880-748-905	Sequence 905, App
26	479	84.6	251	9	US-09-880-748-22	Sequence 22, Appl
27	479	84.6	251	9	US-09-880-748-24	Sequence 24, Appl
28	479	84.6	251	9	US-09-880-748-26	Sequence 26, Appl
29	479	84.6	251	9	US-09-880-748-28	Sequence 28, Appl
30	479	84.6	251	9	US-09-880-748-30	Sequence 30, Appl
31	477.5	84.4	104	10	US-09-828-708-6	Sequence 6, Appl1
32	475	83.9	251	9	US-09-880-748-10	Sequence 10, Appl
33	475	83.9	251	9	US-09-880-748-12	Sequence 12, Appl
34	475	83.9	251	9	US-09-880-748-17	Sequence 17, Appl
35	475	83.9	251	9	US-09-880-748-19	Sequence 19, Appl
36	475	83.9	251	9	US-09-880-748-21	Sequence 21, Appl
37	475	83.9	251	9	US-09-880-748-23	Sequence 23, Appl
38	475	83.9	251	9	US-09-880-748-25	Sequence 25, Appl
39	475	83.9	251	9	US-09-880-748-27	Sequence 27, Appl
40	475	83.9	251	9	US-09-880-748-29	Sequence 29, Appl
41	475	83.9	251	9	US-09-880-748-31	Sequence 31, Appl
42	475	83.9	251	9	US-09-880-748-33	Sequence 33, Appl
43	475	83.9	251	9	US-09-880-748-35	Sequence 35, Appl
44	475	83.9	251	9	US-09-880-748-37	Sequence 37, Appl
45	475	83.9	251	9	US-09-880-748-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1
US-09-848-798-178
Sequence 178, Application US/09848798
Publication No. US20030040605A1
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/848,798
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 178
LENGTH: 108
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH52
US-09-848-798-178
Query Match 95.1%; Score 538; DB 9; Length 108;
Best Local Similarity 97.1%; Pred. No. 1.4e-31;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 4 LTQSPGTLISLSPGERATLSCRAQSQSVSSYLAWYQKPGAPRIILYGAFSRANGIDRF 63
Db 3 LTQSPGTLISLSPGERATLSCRAQSQSVSSYLAWYQKPGAPRIILYGAFSRANGIDRF 62
QY 64 SGSSGTDFTLTISRLPEDPAYVYCCQYSSGPTFGQTKVEIK 108
Db 63 SGSSGTDFTLTISRLPEDPAYVYCCQYSSGPTFGQTKVEIK 107
RESULT 2
US-09-880-748-1499
Sequence 1499, Application US/09880748
Publication No. US20030059937A1

XX Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
 KW envelope glycoprotein; gp120; diagnosis.
 XX
 OS Homo sapiens.
 XX
 PN WO200100678-A1.
 XX
 PD 04-JAN-2001.
 XX
 PF 23-JUN-2000; 2000MO-US17327.
 XX
 PR 30-JUN-1999; 99US-0141701.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Mackinn BA, Reitz MS;
 XX
 DR WPI; 2001-112438/12.
 XX
 PS PDB; AAF29071.
 XX
 PT Novel human monoclonal antibody immunoreactive with human
 PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
 PT in biological sample and providing passive immunotherapy to HIV-1
 PT infected mammal .
 XX
 PS Claim 1; Page 66; 81pp; English.
 XX
 CC The present invention provides the protein and coding sequences for the
 CC variable regions of human monoclonal antibodies which are immunoreactive
 CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
 CC These can be used in diagnosis and therapy of HIV-1 infection.
 CC
 SQ Sequence 108 AA;
 Query Match 95.2%; Score 539; DB 22; Length 108;
 Best Local Similarity 96.3%; Pred. No. 1.7e-33;
 Matches 103; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 2 IYVLTQSPGTLISLSPERATISCRASQSVSSYLAWYQOKPGQAPRLIYGAFSRATGIPD 61
 DB 1 IYVLTQSPGTLISLSPERATISCRASQSVSSYLAWYQOKPGQAPRLIYGAFSRATGIPD 60
 QY 62 RFSGSGSGTDFTLTISRLEPEDFAVYYCQYQSSPMTFGQGTKEIK 108
 DB 61 RFSGSGSGTDFTLTISRLEPEDFAVYYCQYQSSPMTFGQGTKEIK 107
 RE 6
 AAM24101
 ID AAM24101 standard; Protein; 384 AA.
 XX
 AC AAM24101;
 XX
 DT 12-OCT-2001 (first entry)
 DE Human EST encoded protein SEQ ID NO: 1626.
 XX
 KW Human; sheep; pig; cow; fruit fly; Yeast; hamster; macaque; horse;
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
 KW diagnostics; forensic test; gene mapping; genetic disorder;
 KW biodiversity; gene therapy; nutrition.
 XX
 OS Homo sapiens.
 XX
 PN WO200154477-A2.
 XX
 PD 02-AUG-2001.
 XX
 PF 25-JAN-2001; 2001WO-US02687.
 XX
 PR 25-JAN-2000; 2000US-0491404.
 PT 17-JUL-2000; 2000US-0617746.

PR 03-AUG-2000; 2000US-0631451.
 PR 15-SEP-2000; 2000US-0663870.
 XX
 PA (HYSE-) HXSEQ INC.
 XX
 PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Aundi V;
 PI Cao Y, Drmanac RA, Zhang J, Wehrman T;
 XX
 DR WPI; 2001-476164/51.
 XX
 DR N-PSDB; AAH98760.
 XX
 PT Isolated polypeptide for treatment of diseases, diagnostics, raising
 PT antibodies and research use -
 XX
 PS Claim 20; Page 1102-1103; 1275pp; English.
 XX
 CC The present invention provides the protein and coding sequences of novel
 CC proteins from a variety of organisms, including human, dog, cat, horse,
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
 CC from the organism of interest. They can be used in diagnostics,
 CC forensics, gene mapping, identification of mutations, to assess
 CC biodiversity and for nutritional purposes. The present sequence is a
 CC protein of the invention.
 XX
 SQ Sequence 384 AA;
 Query Match 95.2%; Score 539; DB 22; Length 384;
 Best Local Similarity 97.2%; Pred. No. 5.1e-33;
 Matches 105; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 EYVLTQSPGTLISLSPERATISCRASQSVSSYLAWYQOKPGQAPRLIYGAFSRATGIP 60
 DB 167 EYVLTQSPGTLISLSPERATISCRASQSVSSYLAWYQOKPGQAPRLIYGAFSRATGIP 226
 QY 61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQYQSSPMTFGQGTKEIK 108
 DB 227 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQYQSSPMTFGQGTKEIK 274
 RESULT 7
 AAG93666
 ID AAG93666 standard; Protein; 108 AA.
 XX
 AC AAG93666;
 XX
 DT 14-SEP-2001 (first entry)
 DE Human anti-Rh(D) antibody clone SH52 protein sequence.
 XX
 KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 KW red blood cell; Rh phenotype; diagnosis; therapeutic.
 XX
 OS Homo sapiens.
 XX
 PN US6255455-B1.
 XX
 PD 03-JUL-2001.
 XX
 PF 29-JAN-1999; 99US-0240274.
 XX
 PR 11-OCT-1996; 96US-0028550.
 PR 10-APR-1998; 98US-0081380.
 PR 27-JUN-1997; 97US-0884045.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 XX
 PI Siegel DJ;
 XX
 DR WPI; 2001-388931/41.
 DR N-PSDB; AAH68723.
 XX
 PT New isolated protein, preferably a human anti-Rh(D) antibody for use in

PR 26-MAY-2000; 2000US-0579808.
PR 18 SEP 2000 0555Z
DE 18 SEP 2000 0555Z

QY 61 DRFGSGSGTDFLTITSLRLEPDPFAVYCCOYGSSPMTFGGKTVEIK 108
 DB 61 DRFGSGSGTDFLTITSLRLEPDPFAVYCCOYGSSPMTFGGKTVEIK 108

RESULT 2

Q9UL86 PRELIMINARY; PRT; 109 AA.
 ID 09UL86 AC
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Myosin-reactive immunoglobulin kappa chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN 11
 RP SEQUENCE FROM N.A.
 RX DLIN=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 RT EMBL; AF035028; AAD56264.1; -
 DR HSSP; P80362; IWTL.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 109
 SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;
 Query Match 89.2%; Score 505; DB 4; Length 109;
 Best Local Similarity 91.7%; Pred. No. 1.9e-47;
 Matches 99; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
 QY 1 EIVTOSPGTSLSPGRATLSCASQSVSSYLAWYQKPGQAPRLIYGAFSRATGIP 60
 DB 1 EIVTOSPGTSLSPGRATLSCASQSVSSYLAWYQKPGQAPRLIYGAFSRATGIP 60
 QY 61 DRFGSGSGTDFLTITSLRLEPDPFAVYCCOYGSSPMTFGGKTVEIK 108
 DB 61 DRFGSGSGTDFLTITSLRLEPDPFAVYCCOYGSSPMTFGGKTVEIK 108
 RES. 3
 Q9UL83 PRELIMINARY; PRT; 108 AA.
 ID 09UL83 AC
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 RT EMBL; AF035031; AAD56267.1; -
 DR HSSP; P80362; IWTL.
 DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 108
 SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match 77.3%; Score 437.5; DB 4; Length 108;
 Best Local Similarity 81.5%; Pred. No. 4.2e-40;
 Matches 88; Conservative 8; Mismatches 11; Indels 1; Gaps 1;

QY 1 EIVTOSPGTSLSPGRATLSCASQSVSSYLAWYQKPGQAPRLIYGAFSRATGIP 60
 DB 1 EIVTOSPGTSLSPGRATLSCASQSVSSYLAWYQKPGQAPRLIYGAFSRATGIP 59
 QY 61 DRFGSGSGTDFLTITSLRLEPDPFAVYCCOYGSSPMTFGGKTVEIK 108
 DB 60 ARFGSGSGTDFLTITSLRLEPDPFAVYCCOYNNWPTFGGKTVEIK 107

RESULT 4

Q9UL85 PRELIMINARY; PRT; 109 AA.
 ID 09UL85 AC
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Myosin-reactive immunoglobulin kappa chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 RT EMBL; AF035029; AAD56265.1; -
 DR HSSP; P80362; IWTL.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 109
 SQ SEQUENCE 109 AA; 11761 MW; FB1843E7C7AFACCC CRC64;
 Query Match 76.5%; Score 433; DB 4; Length 109;
 Best Local Similarity 80.7%; Pred. No. 1.3e-39;
 Matches 88; Conservative 8; Mismatches 11; Indels 2; Gaps 2;
 QY 1 EIVTOSPGTSLSPGRATLSCASQSVSSYLAWYQKPGQAPRLIYGAFSRATGIP 60
 DB 1 EIVTOSPGTSLSPGRATLSCASQSVSSYLAWYQKPGQAPRLIYGAFSRATGIP 59
 QY 61 DRFGSGSGTDFLTITSLRLEPDPFAVYCCOYGSSPMTFGGKTVEIK 108
 DB 60 ARFGSGSGTDFLTITSLRLEPDPFAVYCCOYNNWPTFGGKTVEIK 108
 RESULT 5
 Q9UL77 PRELIMINARY; PRT; 108 AA.
 ID 09UL77 AC
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region (Fragment).

db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQOKPGAPRLITYGASSRATGIP 60

```

RESULT 2
KV3L_HUMAN          STANDARD;          PRT;          129 AA.
ID   P18135;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG kappa chain V-III region HAH precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88171307; PubMed=3127527;
RT   Kippe T.J., Tomhave E., Chen P.P., Carson D.A.;
RT   "Antibody-associated kappa light chain variable region gene
RT   expressed in chronic lymphocytic leukemia with little or no somatic
RT   mutation. Implications for etiology and immunotherapy.";
RL   Exp. Med. 167:840-852(1988).
CC   1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC   AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC   LEUKEMIA.
DR   HSP; P80362; K3HUA.
DR   InterPro: IPR003006; IG_MHC.
DR   InterPro: IPR003596; IG_V.
DR   Pfam: PF00047; IgV_1.
DR   SMART; SM00406; IgV_1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL          1          20
FT   CHAIN           21         129
FT   DOMAIN          21         43
FT   DOMAIN          44         55
FT   DOMAIN          56         70
FT   DOMAIN          71         77
FT   DOMAIN          78         109
FT   DOMAIN          110        118
FT   DOMAIN          119        129
FT   DISULFID        43         109
FT   NON_TER         129
SQ   SEQUENCE      129 AA; 14073 MW; D3C55292772774D0 CRC64;

Query Match          94.5%; Score 535; DB 1; Length 129;
Best Local Similarity 96.3%; Pred. No. 2,1e-46;
Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY   1 EIVLTGSPGTLSPGERATLSCRASQSVSSSYLAWYQKQKGAAPRLIYGAFSRATGIP 60
DB   21 EIVLTGSPGTLSPGERATLSCRASQSVSSSYLAWYQKQKGAAPRLIYGAFSRATGIP 80
QY   61 DRFGSGSGTDFTLTISRLEPEDPAVYCCQYGSPPWTFGGTKVEIK 108
DB   81 DRFGSGSGTDFTLTISRLEPEDPAVYCCQYGSPPWTFGGTKVEIK 128

RESULT 3
KV3B_HUMAN          STANDARD;          PRT;          109 AA.
ID   P01620;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG kappa chain V-III region SIE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=82046598; PubMed=6794615;
RA   Andrews D.W., Capra J.D.;
RT   "Amino acid sequence of the variable regions of light chains from two
RT   "

```

```

RT   Idiotypically cross-reactive human IGM anti-gamma-globulins of the Wa
RT   group.";
RL   Biochemistry 20:5816-5822(1981).
CC   1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC   GLOBULIN ACTIVITY.
DR   PIR; A01892; K3HUS1.
DR   HSP; P80362; 1WTL.
DR   InterPro: IPR003006; IG_MHC.
DR   InterPro: IPR003596; IG_V.
DR   Pfam; PF00047; IgV_1.
DR   SMART; SM00406; IgV_1.
KW   Immunoglobulin V region.
FT   DISULFID        23         89
FT   NON_TER         109
SQ   SEQUENCE      109 AA; 11775 MW; 7689C3ECDD646FFB4 CRC64;

Query Match          93.5%; Score 529; DB 1; Length 109;
Best Local Similarity 94.4%; Pred. No. 7.2e-48;
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY   1 EIVLTGSPGTLSPGERATLSCRASQSVSSSYLAWYQKQKGAAPRLIYGAFSRATGIP 60
DB   1 EIVLTGSPGTLSPGERATLSCRASQSVSSSYLAWYQKQKGAAPRLIYGAFSRATGIP 60
QY   61 DRFGSGSGTDFTLTISRLEPEDPAVYCCQYGSPPWTFGGTKVEIK 108
DB   61 DRFGSGSGTDFTLTISRLEPEDPAVYCCQYGSPPWTFGGTKVEIK 108

RESULT 4
KV3D_HUMAN          STANDARD;          PRT;          109 AA.
ID   P01632;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG kappa chain V-III region TI.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=72188439; PubMed=5027703;
RA   Suter L., Bernikol H.O., Watanabe S., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
RT   T1). IV. The complete amino acid sequence and its significance for
RT   the mechanism of antibody production.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
CC   1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01895; K3HUT1.
DR   HSP; P80362; 1WTL.
DR   InterPro: IPR003006; IG_MHC.
DR   InterPro: IPR003596; IG_V.
DR   Pfam; PF00047; IgV_1.
DR   SMART; SM00406; IgV_1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DISULFID        23         89
FT   NON_TER         109
SQ   SEQUENCE      109 AA; 8C350586DC7749BC CRC64;

Query Match          91.9%; Score 520; DB 1; Length 109;
Best Local Similarity 93.5%; Pred. No. 6.1e-47;
Matches 101; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY   1 EIVLTGSPGTLSPGERATLSCRASQSVSSSYLAWYQKQKGAAPRLIYGAFSRATGIP 60
DB   1 EIVLTGSPGTLSPGERATLSCRASQSVSSSYLAWYQKQKGAAPRLIYGAFSRATGIP 60
QY   61 DRFGSGSGTDFTLTISRLEPEDPAVYCCQYGSPPWTFGGTKVEIK 108
DB   61 DRFGSGSGTDFTLTISRLEPEDPAVYCCQYGSPPWTFGGTKVEIK 108

```

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:57:42 ; Search time 21.2211 Seconds
(without alignments)
211.085 Million cell updates/sec

Title: US-09-644-668a-7
Perfect score: 566

Sequence: 1 EIVLTQSPGTLISLSPGERAT.....CQYSSSPWTFGQGTKEIK 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	546	96.5	129 1	KV3M_HUMAN
2	535	94.5	129 1	KV3L_HUMAN
3	529	93.5	109 1	KV3B_HUMAN
4	520	91.9	109 1	KV3D_HUMAN
5	515	91.0	109 1	KV3E_HUMAN
6	500	88.9	108 1	KV3A_HUMAN
7	469	88.3	109 1	KV3C_HUMAN
8	466.5	82.9	100 1	KV3G_HUMAN
9	466.5	81.3	128 1	KV3K_HUMAN
10	460	82.4	129 1	KV3H_HUMAN
11	452	79.9	109 1	KV3F_HUMAN
12	419.5	74.1	115 1	KV3I_HUMAN
13	417.5	73.8	134 1	KV4C_HUMAN
14	414	73.1	116 1	KV3J_HUMAN
15	408.5	72.2	114 1	KV4A_HUMAN
16	392.5	69.3	108 1	KV1M_HUMAN
17	392	69.3	133 1	KV4B_HUMAN
18	391.5	69.2	108 1	KV4R_HUMAN
19	390.5	69.0	108 1	KV1H_HUMAN
20	383.5	67.8	108 1	KV1V_HUMAN
21	383.5	67.8	111 1	KV3O_MOUSE
22	380.5	67.2	108 1	KV1F_HUMAN
23	380.5	67.2	108 1	KV1K_HUMAN
24	378.5	66.9	111 1	KV3Q_MOUSE
25	377.5	66.7	108 1	KV1B_HUMAN
26	375.5	66.3	111 1	KV3M_MOUSE
27	374.5	66.2	108 1	KV1Y_HUMAN
28	372.5	65.8	107 1	KV1L_HUMAN
29	372	65.7	107 1	KV1J_HUMAN
30	371.5	65.6	111 1	KV1D_HUMAN
31	369.5	65.3	111 1	KV3N_MOUSE
32	369	65.2	110 1	KV3P_MOUSE
33	368.5	65.1	108 1	KV1O_HUMAN

34	368.5	65.1	129 1	KV1W_HUMAN	P04431 homo sapien
35	368.5	65.1	131 1	KV1I_MOUSE	P01661 mus musculus
36	367.5	64.9	108 1	KV1E_HUMAN	P01597 homo sapien
37	367.5	64.9	108 1	KV1N_HUMAN	P01606 homo sapien
38	366.5	64.8	111 1	KV3H_MOUSE	P01617 homo sapien
39	366	64.7	113 1	KV2D_HUMAN	P01617 homo sapien
40	365	64.5	117 1	KV2E_HUMAN	P06309 homo sapien
41	363.5	64.2	111 1	KV3A_MOUSE	P01654 mus musculus
42	363.5	64.2	111 1	KV3C_MOUSE	P01654 mus musculus
43	361.5	63.9	108 1	KV1O_HUMAN	P01654 mus musculus
44	360.5	63.7	112 1	KV3G_MOUSE	P01659 mus musculus
45	359.5	63.5	111 1	KV3J_MOUSE	P01662 mus musculus

ALIGNMENTS

RESULT 1
KV3M_HUMAN STANDARD; PRT; 129 AA.

AC P18136;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 19 kappa chain V-III region HIC precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kippa T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Antibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC - DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCTIC
CC LEUKEMIA.

DR PIR; P18021; KAHMT.
DR HSSP; P80362; IWT.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IG_1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129
FT DOMAIN 21 43
FT DOMAIN 44 55
FT DOMAIN 56 70
FT DOMAIN 71 77
FT DOMAIN 78 109
FT DOMAIN 110 118
FT DOMAIN 119 129
FT DISULFID 43 109
FT NON_TER 129
SQ SEQUENCE 129 AA; 14070 MW; 7395528E2B74D6 CRC64;

Query Match 96.5%; Score 546; DB 1; Length 129;
Best Local Similarity 97.2%; Pred. No. 1.5e-49;
Matches 105; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSYLAHQPGAPRLITYGAFSRATGIP 60
DB 21 EIVLTQSPGTLISLSPGERATLSCRASQSVSSYLAHQPGAPRLITYGAFSRATGIP 80
QY 61 DRSSGSGSDFTLTISRLPEPDAFYVYCOYGGSPWTFGQGTKEIK 108
DB 81 DRSSGSGSDFTLTISRLPEPDAFYVYCOYGGSPWTFGQGTKEIK 128

C/Keywords: autoantibody; chronic lymphocytic leukemia; heterotrimer; immunoglobulin
 F/1-20/Domain: signal sequence #status predicted <SIG>
 F/21-129/Product: Ig kappa chain V-III region (Hic) #status predicted <MAT>
 F/21-117/Region: V segment
 F/36-111/Domain: immunoglobulin homology <IMM>
 F/44-55/Region: complementarity-determining 1
 F/71-77/Region: complementarity-determining 2
 F/110-117/Region: complementarity-determining 3
 F/118-129/Region: segment J (UKL)
 F/43-109/Disulfide bonds: #status predicted

Query Match 96.5%; Score 546; DB 1; Length 129;
 Best Local Similarity 97.2%; Pred. No. 8.6e-39;
 Matches 105; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 21 EIVTQSPGTLISPGERATLSCRASQSVSSSYLAWYQKRGQAPRLIYGASRATGIP 60
 |||||
 1 EIVTQSPGTLISPGERATLSCRASQSVSSSYLAWYQKRGQAPRLIYGASRATGIP 60

Qy 61 DRFGSGSGTDFTLTISRLEPEDPAVYCCQYGSPPFTFGQTKVEIK 108
 |||||
 81 DRFGSGSGTDFTLTISRLEPEDPAVYCCQYGSPPFTFGQTKVEIK 128

RESULT 3

Ig kappa chain V-III region (Gar and Flo) - human (fragment)

C/Species: Homo sapiens (man)
 C/Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000

C/Accession: H30601; E30601
 R/Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solc

A/Title: Structural and idiotypic characterization of the L chains of human IGM autoanti
 A/Reference number: A30601; PMID:89215279; PMID:2496160
 A/Accession: H30601

A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-109 <GON1>
 A/Accession: E30601

A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-109 <GON2>
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F/16-91/Domain: immunoglobulin homology <IMM>

Query Match 95.4%; Score 540; DB 2; Length 109;
 Local Similarity 96.3%; Pred. No. 2.3e-38;
 Matches 104; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EIVTQSPGTLISPGERATLSCRASQSVSSSYLAWYQKRGQAPRLIYGASRATGIP 60
 |||||
 1 EIVTQSPGTLISPGERATLSCRASQSVSSSYLAWYQKRGQAPRLIYGASRATGIP 60

Qy 61 DRFGSGSGTDFTLTISRLEPEDPAVYCCQYGSPPFTFGQTKVEIK 108
 |||||
 61 DRFGSGSGTDFTLTISRLEPEDPAVYCCQYGSPPFTFGQTKVEIK 108

RESULT 4

Ig kappa chain V-III region (Gio) - human (fragment)

C/Species: Homo sapiens (man)
 C/Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000

C/Accession: B30601
 R/Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solc

A/Title: Structural and idiotypic characterization of the L chains of human IGM autoanti
 A/Reference number: A30601; PMID:89215279; PMID:2496160
 A/Accession: B30601

A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-109 <GON>

C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F/16-91/Domain: immunoglobulin homology <IMM>

Query Match 95.2%; Score 539; DB 2; Length 109;
 Best Local Similarity 97.2%; Pred. No. 2.8e-38;
 Matches 105; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVTQSPGTLISPGERATLSCRASQSVSSSYLAWYQKRGQAPRLIYGASRATGIP 60
 |||||
 1 EIVTQSPGTLISPGERATLSCRASQSVSSSYLAWYQKRGQAPRLIYGASRATGIP 60

Qy 61 DRFGSGSGTDFTLTISRLEPEDPAVYCCQYGSPPFTFGQTKVEIK 108
 |||||
 61 DRFGSGSGTDFTLTISRLEPEDPAVYCCQYGSPPFTFGQTKVEIK 108

RESULT 5

Ig kappa chain V-III region (Cur) - human (fragment)

C/Species: Homo sapiens (man)
 C/Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000

C/Accession: D30601
 R/Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solc

A/Title: Structural and idiotypic characterization of the L chains of human IGM autoanti
 A/Reference number: A30601; PMID:89215279; PMID:2496160
 A/Accession: D30601

A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-109 <GON>
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F/16-91/Domain: immunoglobulin homology <IMM>

Query Match 95.1%; Score 538; DB 2; Length 109;
 Best Local Similarity 97.2%; Pred. No. 3.4e-38;
 Matches 105; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVTQSPGTLISPGERATLSCRASQSVSSSYLAWYQKRGQAPRLIYGASRATGIP 60
 |||||
 1 EIVTQSPGTLISPGERATLSCRASQSVSSSYLAWYQKRGQAPRLIYGASRATGIP 60

Qy 61 DRFGSGSGTDFTLTISRLEPEDPAVYCCQYGSPPFTFGQTKVEIK 108
 |||||
 61 DRFGSGSGTDFTLTISRLEPEDPAVYCCQYGSPPFTFGQTKVEIK 108

RESULT 6

Ig kappa chain V-III region (Pay) - human (fragment)

C/Species: Homo sapiens (man)
 C/Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000

C/Accession: C30601
 R/Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solc

A/Title: Structural and idiotypic characterization of the L chains of human IGM autoanti
 A/Reference number: A30601; PMID:89215279; PMID:2496160
 A/Accession: C30601

A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-109 <GON>
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F/16-91/Domain: immunoglobulin homology <IMM>

Query Match 94.7%; Score 536; DB 2; Length 109;
 Best Local Similarity 96.3%; Pred. No. 5e-38;
 Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVTQSPGTLISPGERATLSCRASQSVSSSYLAWYQKRGQAPRLIYGASRATGIP 60
 |||||
 1 EIVTQSPGTLISPGERATLSCRASQSVSSSYLAWYQKRGQAPRLIYGASRATGIP 60

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 17:11:36 ; Search time 33.3474 Seconds

(without alignments)
311.344 Million cell updates/sec

Title: US-09-644-668a-7

Perfect score: 566

Sequence: 1 EIVLTGSPGTLSPGRAT.....COYGSSEPTGQTKVEIK 108

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

To: Number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

1: PIR 73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	549	97.0	108 2 C30608	ig kappa chain V-I
2	546	96.5	129 1 K3H0H1	ig kappa chain pre
3	540	95.4	109 2 H30601	ig kappa chain V-I
	539	95.2	109 2 B30601	ig kappa chain V-I
	538	95.1	109 2 D30601	ig kappa chain V-I
	536	94.7	109 2 C30601	ig kappa chain V-I
7	535	94.5	129 1 K3H0H1	ig kappa chain pre
8	533	94.2	109 2 G30601	ig kappa chain V-I
9	532	94.0	109 2 PH0963	ig kappa chain V-I
10	531	93.8	109 2 A30608	ig kappa chain V-I
11	531	93.8	109 2 S49532	ig kappa chain V-I
12	531	93.6	129 2 S49532	ig kappa chain V-I
13	530	93.6	129 2 S49532	ig kappa chain V-I
14	530	93.6	129 2 S49532	ig kappa chain V-I
15	529	93.5	109 1 K3H0H1	ig kappa chain pre
16	528.5	93.4	109 1 S49532	ig kappa chain V-I
17	525	92.8	107 2 PH0963	ig kappa chain V-I
18	525	92.8	109 2 G30607	ig kappa chain V-I
19	524	92.6	109 2 F30601	ig kappa chain V-I
20	524	92.6	109 2 S20636	ig kappa chain V-I
21	520	91.9	109 1 K3H0H1	ig kappa chain pre
22	515	91.0	109 1 K3H0H1	ig kappa chain pre
23	515	91.0	109 1 K3H0H1	ig kappa chain pre
24	513	90.6	108 2 B30608	ig kappa chain V-I
25	510.5	90.2	121 2 S40327	ig kappa chain V-I
26	510	89.9	110 2 E30607	ig kappa chain V-I
27	509	89.9	109 2 S20633	ig kappa chain V-I
28	508.5	89.8	108 2 H44151	ig kappa chain V-I

30	506	89.4	129 2 A32274	ig kappa chain pre
31	503	88.9	108 1 K3H0H1	ig kappa chain V-I
32	503	88.9	215 2 J50242	ig kappa chain V-I
33	502	88.7	130 2 S20637	ig kappa chain V-I
34	501.5	88.6	110 2 S44120	ig kappa chain V-I
35	500	88.3	109 1 K3H0H1	ig kappa chain pre
36	500	88.3	108 2 K3H0H1	ig kappa chain pre
37	499.5	88.3	108 2 E30609	ig kappa chain V-I
38	497	87.8	109 2 S47181	ig kappa chain V-I
39	495.5	87.5	104 2 PH0964	ig kappa chain V-I
40	495.5	87.5	129 2 S40325	ig kappa chain V-I
41	486.5	86.0	111 2 S23628	ig kappa chain V-I
42	485	85.7	96 2 A30601	ig kappa chain V-I
43	485	85.7	116 2 B27594	ig kappa chain V-I
44	485	85.7	215 2 A23746	ig kappa chain V-I
45	483	85.3	108 2 S33988	ig kappa chain V-I

ALIGNMENTS

RESULT 1

ig kappa chain V-III region (Pie) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000

C/Accession: C30608

R/Gonl, F.R.; Chen, P.P.; McGinnis, D.; Arjona, M.L.; Fernandez, J.; Carson, D.; S.

J. Immunol. 142, 3158-3163, 1989

A/Title: Structural and idiotypic characterization of the L chains of human IgM autoantibodies

A/Reference number: A30601; PMID:89215279; PMID:2496160

A/Accession: C30608

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-108 <GON>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/16-91/Domain: immunoglobulin homology <IMV>

Query Match

Best Local Similarity 97.0%; Score 549; DB 2; Length 108;

Matches 105; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 1 EIVLTGSPGTLSPGRATLSCASOSVSYAWOQKPGAPRLIYASFRATGIP 60

QY 61 DRFGSGSGTDFTLTISRLPEDEFAVYCCOYGSSEPTGQTKVEIK 108

Db 61 DRFGSGSGTDFTLTISRLPEDEFAVYCCOYGSSEPTGQTKVEIK 108

RESULT 2

ig kappa chain precursor V-III region (Hic) - human

C/Species: Homo sapiens (man)

C/Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 21-Jan-2000

C/Accession: P10021

R/Klips, T.J.; Tomhave, E.; Chen, P.P.; Carson, D.A.

J. Exp. Med. 167, 840-852, 1988

A/Title: Autoantibody-associated kappa light chain variable region gene expressed in c

A/Reference number: P10021; PMID:88171307; PMID:3127527

A/Accession: P10021

A/Molecule type: mRNA

A/Residues: 1-119 <KIP>

C/Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed

A/Genes: GDB:136266

A/Cross-references: GDB:136266

A/Map position: 2p12-2p11

C/Complex: An immunoglobulin heterotrimer subunit consists of two identical light (k) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into

C/Superfamily: immunoglobulin V region; immunoglobulin homology

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 17:11:36 ; Search time 2.1614 Seconds

(without alignments)
311.344 Million cell updates/sec

Title: US-09-644-668A-29

Perfect score: 34

Sequence: 1 GAFSRAT 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 73:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	31	91.2	165 2	S08641
2	31	91.2	228 2	S32563
3	31	91.2	603 2	E84744
4	30	88.2	72 2	T17585
5	30	88.2	185 2	AE2388
6	30	88.2	2352 2	T43431
7	29	85.3	200 2	T46222
8	29	85.3	307 2	C75584
9	29	85.3	396 1	YTRC32
10	29	85.3	752 2	G82798
11	29	85.3	1084 2	B70588
12	29	85.3	1461 2	S40328
13	28	82.4	131 2	S40328
14	28	82.4	173 2	C95850
15	28	82.4	316 2	P71338
16	28	82.4	351 2	AD1079
17	27	79.4	164 2	AD0813
18	27	79.4	199 2	AB3585
19	27	79.4	209 2	JC7239
20	27	79.4	223 2	S73367
21	27	79.4	309 2	A12378
22	27	79.4	311 2	F70184
23	27	79.4	420 2	AH3015
24	27	79.4	425 2	G98268
25	27	79.4	2067 2	A42854
26	26	76.5	34 2	H30607
27	26	76.5	54 2	A40381
28	26	76.5	54 2	A25521
29	26	76.5	62 2	I30601

30	26	76.5	83 2	I30607	Ig kappa chain V-I
31	26	76.5	87 2	S16843	Ig kappa chain V-I
32	26	76.5	87 2	S16823	Ig kappa chain V-I
33	26	76.5	89 2	S34096	Ig kappa chain V-I
34	26	76.5	91 2	S37520	Ig kappa chain V-I
35	26	76.5	91 2	S67940	Ig kappa chain V-I
36	26	76.5	92 2	S37524	Ig kappa chain V-I
37	26	76.5	92 2	S37513	Ig kappa chain V-I
38	26	76.5	92 2	S37519	Ig kappa chain V-I
39	26	76.5	92 2	S37517	Ig kappa chain V-I
40	26	76.5	92 2	S37514	Ig kappa chain V-I
41	26	76.5	92 2	S37510	Ig kappa chain V-I
42	26	76.5	92 2	S37518	Ig kappa chain V-I
43	26	76.5	93 2	S37526	Ig kappa chain V-I
44	26	76.5	93 2	S37528	Ig kappa chain V-I
45	26	76.5	96 2	A30601	Ig kappa chain V-I

ALIGNMENTS

RESULT 1
S08641
hypothetical protein 2 - zebra fish
C/Species: Brachydanio rerio (zebra fish)
C/Date: 21-Nov-1993 #sequence_revision 26-May-1995 #text_change 15-Oct-1999
C/Accession: S08641
R/Molstad, P.R.; Molven, A.; Apold, J.; Fjose, A.
EMBO J. 9, 515-524, 1990
A/Title: The zebrafish homeobox gene hox-2.2: transcription unit, potential regulatory
A/Reference number: S086339; M01D:90151628; PMID:1968004
A/Accession: S08641
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-165 <MO>
A/Cross-references: EMBL:X17267
C/Species: Brachydanio rerio (zebra fish)
C/Date: 08-Dec-1993 #sequence_revision 26-May-1995 #text_change 24-Sep-1999
C/Accession: S32563; S08642; S25594
R/Molven, A.; Hordvik, I.; Njorstad, P.R.
Biochim. Biophys. Acta 1173, 102-106, 1993
A/Title: Sequence analysis of the zebrafish hox-B5/B6 region.
A/Reference number: S32563; M01D:93250038; PMID:8097929
A/Accession: S32563
A/Molecule type: DNA
A/Residues: 1-228 <MO>
A/Cross-references: EMBL:X68248; NID:g62535; PID:CAA48319.1; PID:g62536
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
A/Note: only a small part of the coding sequence given
R/Molstad, P.R.; Molven, A.; Apold, J.; Fjose, A.
EMBO J. 9, 515-524, 1990
A/Title: The zebrafish homeobox gene hox-2.2: transcription unit, potential regulatory
A/Reference number: S086339; M01D:90151628; PMID:1968004
A/Accession: S08642
A/Molecule type: DNA
A/Residues: 1-228 <MO>

Query Match 91.2% Score 31; DB 2; Length 165;
Best Local Similarity 85.7% Pred. No. 8.1;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAFSRAT 7
Db 72 GAFSRAT 78
RESULT 2
S32563
homeotic protein Hox-B6 - zebra fish
N/Alternate names: homeotic protein Hox 2.2
C/Species: Brachydanio rerio (zebra fish)
C/Date: 08-Dec-1993 #sequence_revision 26-May-1995 #text_change 24-Sep-1999
C/Accession: S32563; S08642; S25594
R/Molven, A.; Hordvik, I.; Njorstad, P.R.
Biochim. Biophys. Acta 1173, 102-106, 1993
A/Title: Sequence analysis of the zebrafish hox-B5/B6 region.
A/Reference number: S32563; M01D:93250038; PMID:8097929
A/Accession: S32563
A/Molecule type: DNA
A/Residues: 1-228 <MO>
A/Cross-references: EMBL:X68248; NID:g62535; PID:CAA48319.1; PID:g62536
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
A/Note: only a small part of the coding sequence given
R/Molstad, P.R.; Molven, A.; Apold, J.; Fjose, A.
EMBO J. 9, 515-524, 1990
A/Title: The zebrafish homeobox gene hox-2.2: transcription unit, potential regulatory
A/Reference number: S086339; M01D:90151628; PMID:1968004
A/Accession: S08642
A/Molecule type: DNA
A/Residues: 1-228 <MO>

A/Cross-references: EMBL:X17267; NID:G62530; PIDD:CAA35171.1; PID:G313688
 C/Genetics:
 A/Gene: Hox-B6, Hox 2.2
 A/Introns: 144/1
 C/Superfamily: unassigned homeobox proteins; homeobox homology
 C/Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F/151-207/domain: homeobox homology <Hox>

Query Match 91.2%; Score 31; DB 2; Length 228;
 Best Local Similarity 85.7%; Pred. No. 11;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GAFSRAT 7
 Db 64 GAFSRAT 70

RESULT 3
 E84744
 hypothetical protein Atg33360 (imported) - Arabidopsis thaliana
 C/Accession: E84744
 C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 R/Lin, X.; Kaul, S.; Roundley, S.D.; Shea, T.P.; Bentio, M.T.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
 Neure, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A/Reference number: AB4420; MUID:20083487; PMID:10617197
 A/Accession: E84744
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-603 <STO>
 A/Cross-references: GB:AE002093; NID:G2459419; PIDD:AA80654.1; GSPDB:GN00139
 C/Genetics:
 A/Gene: Atg33360
 A/Map position: 2

Query Match 91.2%; Score 31; DB 2; Length 603;
 Best Local Similarity 85.7%; Pred. No. 29;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GAFSRAT 7
 Db 64 GAFSRAT 70

RESULT 4
 T46222
 hypothetical protein a95R - Chlorella virus PBCV-1
 C/Species: Chlorella virus PBCV-1
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 R/Graves, M.V.; Van Etten, J.L.
 submitted to the EMBL Data Library, May 1999
 A/Accession: T17585
 A/Reference number: Z18806
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-72 <GRA>
 A/Cross-references: EMBL:U42580; NID:G4028896; PIDD:AA36463.1
 A/Experimental source: specific host Chlorella strain NC64A
 C/Genetics:
 A/Gene: a95R

Query Match 88.2%; Score 30; DB 2; Length 72;
 Best Local Similarity 85.7%; Pred. No. 6.2;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GAFSRAT 7
 Db 36 GAFSRAT 42

RESULT 5

AE2388
 glutathione S-transferase (imported) - Nostoc sp. (strain PCC 7120)
 C/Species: Nostoc sp.
 A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
 C/Accession: AE2388
 R/Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriya,
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
 DNA Res. 8, 205-213, 2001
 A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
 A/Reference number: AB1807; MUID:21595285; PMID:1175840
 A/Accession: AE2388
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-185 <KUR>
 A/Cross-references: GB:BA000019; PIDD:BA676360.1; PID:G17133798; GSPDB:GN00179
 A/Experimental source: strain PCC 7120
 C/Genetics:
 A/Gene: alr4661
 C/Superfamily: hypothetical protein b0838

Query Match 88.2%; Score 30; DB 2; Length 185;
 Best Local Similarity 85.7%; Pred. No. 16;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GAFSRAT 7
 Db 7 GAFSRAT 13

RESULT 6

T43431
 alpha-glucan synthase (EC 2.4.1.-) mok12 - fission yeast (Schizosaccharomyces pombe)
 N/Alternate names: morphological/kinase-inhibitor supersensitive protein mok12
 C/Species: Schizosaccharomyces pombe
 C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
 R/Katayama, S.; Toda, T.
 submitted to the EMBL Data Library, October 1998
 A/Description: Fission yeast alpha-glucan synthase Mok1 localizes closely with actin
 A/Reference number: Z22509
 A/Accession: T43431
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-2352 <KAT>
 A/Cross-references: EMBL:AB018381; PIDD:BA47558.1
 A/Experimental source: strain h-972
 C/Genetics:
 A/Gene: mok12
 C/Function:
 A/Description: involved in cell morphogenesis interdependently of the actin cytoskeleton
 C/Keywords: glycoyltransferase; hexosyltransferase; transmembrane protein

Query Match 88.2%; Score 30; DB 2; Length 2352;
 Best Local Similarity 85.7%; Pred. No. 1.9e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 GAFSRAT 7
 Db 1114 GAFSRAT 1120

RESULT 7

T46222
 hypothetical protein T9C5.40 - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 28-Jul-2000
 C/Accession: T46222
 R/Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Meves, H.W.; Lemcke
 submitted to the Protein Sequence Database, December 1999
 A/Reference number: Z23026

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:57:42 ; Search time 1.37544 Seconds
(without alignments)
211.085 Million cell updates/sec

Title: US-09-644-668a-29

Sequence: 1 GAFSRAT 7

Scoring table: BLOSUM62
Gapop 10.0, Gapept 0.5

Searched: 112892 seqs, 41476328 residues
To: number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	31	91.2	228 1	HXB6_BRARE
2	30	88.2	2352 1	MOKC_SCHPO
3	29	85.3	396 1	TCR3_ECOLI
4	28	82.4	683 1	BGH3_PIG
5	27	79.4	164 1	EUKR_SALTY
6	27	79.4	210 1	PDX5_MOUSE
7	27	79.4	223 1	YB13_MYCPN
8	27	79.4	513 1	DMPI_HUMAN
9	27	79.4	514 1	MURR_PALSO
10	27	79.4	2067 1	BIME_EMENT
11	26	76.5	100 1	KV3C_HUMAN
12	26	76.5	106 1	YFUS_PYRMO
13	26	76.5	109 1	KV3B_HUMAN
14	26	76.5	109 1	KV3E_HUMAN
15	26	76.5	109 1	KV3G_HUMAN
16	26	76.5	123 1	SVS5_RAT
17	26	76.5	129 1	KV3L_HUMAN
18	26	76.5	129 1	KV3M_HUMAN
19	26	76.5	188 1	SP21_SRIAU
20	26	76.5	235 1	UL03_HSV11
21	26	76.5	243 1	AG16_TRYBB
22	26	76.5	251 1	TP1S_PSEAR
23	26	76.5	286 1	FLA2_TREMA
24	26	76.5	304 1	YACR_ECOLI
25	26	76.5	326 1	Y883_PYRHO
26	26	76.5	380 1	FOS_HUMAN
27	26	76.5	381 1	FOS_CRIGR
28	26	76.5	381 1	FOS_MESAU
29	26	76.5	388 1	METB_MYCTU
30	26	76.5	463 1	DNNA_PROS9
31	26	76.5	466 1	VL2_HPVS2
32	26	76.5	477 1	VL2_HP442
33	26	76.5	513 1	FLAB_HBLPY

34	26	76.5	572 1	BLNO_MRYVE	Q12737 myrothecium
35	26	76.5	516 1	MURS_RHIME	P56683 rhizobium m.
36	26	76.5	933 1	PRGR_HUMAN	P06401 homo sapien
37	26	76.5	1088 1	PICO_HUMAN	O81e68 homo sapien
38	26	76.5	1333 1	YN99_YEAST	P53756 saccharomyc
39	26	76.5	1374 1	VCAP_HSV11	P06491 herpes simp
40	26	76.5	4349 1	PAT2_HUMAN	O82577 rattus norv
41	26	76.5	4351 1	PAT2_RAT	P00030 eisenia foe
42	25	73.5	108 1	CYC_EISFO	O82577 rattus norv
43	25	73.5	125 1	YFBJ_SALTY	O82577 rattus norv
44	25	73.5	125 1	YFBJ_SALTY	O82577 rattus norv
45	25	73.5	163 1	PINI_HUMAN	O13526 homo sapien

ALIGNMENTS

RESULT 1
HXB6_BRARE STANDARD; PRT; 228 AA.
AC P15861;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-B6 (ZF-22).
GN HXB6 OR HOXB6 OR Hox-B6 OR ZF-22.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_Taxid=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=90151628; PubMed=1968004;
RA Njolstad P.R., Molven A., Apold J., Fjose A.;
RT "The zebrafish homeobox gene hox-2.2: transcription unit, potential regulatory regions and in situ localization of transcripts";
RL EMBO J. 9:515-524(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93250038; PubMed=8097929;
RA Molven A., Hordvik I., Njolstad P.R.;
RT "Sequence analysis of the zebrafish hox-B5/B6 region";
RL Biochim. Biophys. Acta 1173:102-106(1993).
CC - FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC - SUBCELLULAR LOCATION: Nuclear.
CC - SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@sib-sib.ch).
CC EMBL; X1767; CAA35171.1; -
CC EMBL; X68248; CAA48319.1; -
CC PIR; S08642; S08642.
CC PIR; S25594; S25594.
CC PIR; S32563; S32563.
CC HSBP; P02833; IHOM.
CC TRANSFAC; T03664; -
CC ZFIN; ZDB-GENE-990415-106; hoxb6a.
CC InterPro; IPR001827; Antennapedia.
CC InterPro; IPR001356; Homeobox.
CC Pfam; PF00046; homeobox.1.
CC PRINTS; PR00025; ANTENNAPEDIA.
CC PRINTS; PR00024; HOMEOBOX.
CC Prodom; PD000010; Homeobox.1.

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RA Borzym K, Langerer I., Beck A., Lehrnach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wandt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaue V., Motier S.,
RA Gailberd F., Aves S.-J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucus M., Rochet M., Galliard C., Tallada V.A., Garzon A., Rhode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsberg S.L.,
RA Cerruttl L., Lowe T., McCombie W.R., Palsten I., Fotschkin J.,
RA Shpakovski G.V., Ussery D., Bartell B.G., Nurge P.,
RA "The genome sequence of Schizosaccharomyces pombe."
RL Nature 415:871-880(2002).
CC -I- CATALYTIC ACTIVITY: UDP-glucose + {alpha-D-glucosyl-(1,3)}(N) =
CC UDP + {alpha-D-glucosyl-(1,3)}(N+1)
CC -I- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/ebis/announce/
CC or send an email to license@ebi.ac.uk.)
CC -----
DR EMBL; AB018381; BAA76558.1; -
DR EMBL; AB004534; BAA21388.1; ALT_INIT.
DR EMBL; AL550971; CAC37503.1; -
DR InterPro; IPR000461; Alpha_amlase.
DR InterPro; IPR001296; Glycos_transf_1.
DR Pfam; PF00128; alpha-amyrase; 1.
DR Pfam; PF00534; Glycos_transf_1; 1.
DR Cell wall; Glycosyltransferase; Glycosyltransferase.
DR SEQUENCE 2352 AA; 266561 MW; 78ADF9C2F7140BBA CRC64;
SQ
Query Match 88.2%; Score 30; DB 1; Length 2352;
Best Local Similarity 85.7%; Pred. No. 79;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Cy 1 GAFSPAT 7
Db 1114 GAFSPAT 1120
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RESULT 3
TCR3_ECOLI STANDARD; PRT; 396 AA.
AC P02981;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Tetracycline resistance protein, class C (TET(C)).
GN TET(A).
OS Escherichia coli.
OC Plasmid pBR322.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
CX NCBI_TaxID=562;
CX [1]
CX SEQUENCE FROM N.A.
CX MEDLINE=80002802; PubMed=383387;
CX Sutcliffe J.G.,
CX "Complete nucleotide sequence of the Escherichia coli plasmid
CX pBR322."
CX Cold Spring Harb. Symp. Quant. Biol. 43:77-90(1979).
CX [2]
CX REVISIONS, AND IDENTIFICATION OF PROTEIN.
CX MEDLINE=83117828; PubMed=6337373;
CX Llynen Z.;
CX "Directed mutagenesis method for analysis of mutagen specificity:
CX application to ultraviolet-induced mutagenesis."
CX Proc. Natl. Acad. Sci. U.S.A. 80:237-241(1983).
CX [3]
CX REVISIONS, AND IDENTIFICATION OF PROTEIN.
CX MEDLINE=83263146; PubMed=6307828;

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OM protein - protein search, using sw model

Run on: April 16, 2003, 17:13:59; Search time 7.17193 Seconds
(without alignments)
201.108 Million cell updates/sec

Title: US-09-644-668A-29

Perfect score: 34

Sequence: 1 GAFSRAT 7

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

To: number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

SPREMBL.21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriophage.*
17: sp_archaeal.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	31	91.2	85	10	08QPU3
2	31	91.2	603	12	022787
3	30	88.2	72	12	084416
4	30	88.2	164	11	09CVB3
5	30	88.2	185	16	08YNA6
6	30	88.2	195	17	09HKH3
7	29	85.3	200	10	09S7F8
8	29	85.3	307	16	09RYL0
9	29	85.3	340	2	09KWT8
10	29	85.3	354	11	09QZ29
11	29	85.3	359	4	060759
12	29	85.3	359	11	091VY6
13	29	85.3	396	2	0939B6
14	29	85.3	396	2	091UW6
15	29	85.3	671	2	085671
16	29	85.3	671	2	047867

17	29	85.3	719	16	08XWU4	08xwU4 ralatonia s
18	29	85.3	734	3	08WZU0	08wzU0 neurospora
19	29	85.3	752	16	09PZ25	09pZ25 xyella fas
20	29	85.3	864	10	09LW22	09lW22 oryza sativ
21	29	85.3	1084	16	083423	083423 treponema p
22	29	85.3	1298	12	09WRL9	09wRl9 macaca mula
23	29	85.3	1298	12	09J2G9	09j2G9 macaca mula
24	29	85.3	1461	16	005819	005819 mycobacteri
25	29	85.3	1750	2	09RFX5	09rFX5 stigmella
26	28	82.4	61	12	P89262	P89262 xestia c-ni
27	28	82.4	93	6	09SKM1	09sKml canis faml
28	28	82.4	173	16	092X95	092x95 rhizobium m
29	28	82.4	185	17	097AG3	097ag3 thermoplas
30	28	82.4	270	4	09HBL3	09hBl3 homo sapien
31	28	82.4	275	12	08OND9	08ond9 ectocarpus
32	28	82.4	316	16	083343	083343 treponema p
33	28	82.4	322	3	09CAG7	09cAg7 neurospora
34	28	82.4	360	16	09KX29	09kX29 streptomyce
35	28	82.4	361	16	08YAS8	08yAs8 listeria mo
36	28	82.4	382	2	P96101	P96101 thlobacillu
37	28	82.4	425	4	096G50	096G50 homo sapien
38	28	82.4	478	2	032600	032600 pantoea ag9
39	28	82.4	545	4	096FW7	096fw7 homo sapien
40	28	82.4	701	16	096MT5	096mT5 rhizobium l
41	28	82.4	707	4	096KH1	096Kh1 homo sapien
42	28	82.4	707	4	096CT2	096cT2 homo sapien
43	28	82.4	749	11	09CY92	09cY92 mus musculu
44	28	82.4	786	4	09HWS5	09hW5 homo sapien
45	28	82.4	791	4	096KX8	096Kx8 homo sapien

ALIGNMENTS

RESULT 1	08QPU3	PRELIMINARY;	PRT;	85 AA.
ID	08QPU3			
AC	08QPU3			
DT	01-JUN-2002 (T-EMBLrel. 21, Created)			
DT	01-JUN-2002 (T-EMBLrel. 21, Last sequence update)			
DT	01-JUN-2002 (T-EMBLrel. 21, Last annotation update)			
GN	Putative AC4 protein.			
DN	AC4.			
OS	Tomato Infectious Yellow virus.			
OC	Viruses; ssDNA viruses; Geminiviridae; Begomovirus.			
OX	NCBI_TaxID=172393;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=MG-B11;			
RA	Ribeiro S.G., Ambrozewicz L.P., de Avila A.C., Calegario R.F.,			
RA	Fernandes J.J., Lima M.F., Mello R.N., Rocha H., Zarbini F.M.;			
RT	Distribution and genetic diversity of tomato-infecting geminiviruses			
RT	in Brazil.			
RL	Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AY049208; AAL82834.1;			
SO	SEQUENCE 85 AA; 9571 MW; 910BBS394CD829A3 CRC64;			
Query Match	91.2%;	Score 31;	DB 12;	Length 85;
Best Local Similarity	85.7%;	Pred. No. 13;		
Matches	6;	Conservative	1;	Mismatches
			0;	Indels
			0;	Gaps
Qy	1 GAFSRAT 7			
Db	61 GAFSRAT 67			
RESULT 2	022787	PRELIMINARY;	PRT;	603 AA.
ID	022787			
AC	022787			
DT	01-JUN-1998 (T-EMBLrel. 05, Created)			
DT	01-JUN-1998 (T-EMBLrel. 05, Last sequence update)			
DT	01-DEC-2001 (T-EMBLrel. 19, Last annotation update)			

DE ATG33360 protein.
 GN Arabidopsis thaliana (Mouse-ear cross).
 OS Arabidopsis thaliana (Mouse-ear cross).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC euroside II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.J., Romling C.M., Koo H., Moffat K.S.,
 RA Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,
 RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
 RA Copenhagen G.P., Preuss D., Niernman W.C., White O., Eisen J.A.,
 RA Salzberg S.L., Fraser C.M., Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 thaliana";
 RL Nature 402:761-768 (1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Lin X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC002332; AB80654.1;
 SQ SEQUENCE 603 AA; 66507 MW; 613A6A4863FC7462 CRC64;
 Query Match
 Best Local Similarity 91.2%; Score 31; DB 10; Length 603;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GAFSRAT 7
 Db 64 GFSRAT 70
 RESULT 3
 ID Q84416 PRELIMINARY; PRT; 72 AA.
 AC Q84416;
 DT 01-NOV-1996 (TRENBLrel. 01. Created)
 DT 01-NOV-1996 (TRENBLrel. 01. Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19. Last annotation update)
 DE A9SR protein.
 GN A9SR.
 OS Paramesitium bursaria chlorella virus 1 (PBCV-1).
 OC Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Chlorovirus.
 NCBI_TaxID=10506;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95407089; PubMed=7676624;
 RA Li Y., Lu Z., Burbank D.E., Kutish G.F., Rock D.L., Van Etten J.L.;
 RT "Analysis of 43 kb of the Chlorella virus PBCV-1 330-kb genome: map
 positions 45 to 88";
 RL Virology 212:134-150 (1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20013326; PubMed=10544099;
 RA Kaiser A., Vollmert M., Tholl D., Graves M.V., Gurnon J.R., Xing W.,
 RA Lasec A.D., Nickerson K.W., Van Etten J.L.;
 RT "Chlorella virus PBCV-1 encodes a functional homosperrmidine
 synthase";
 RL Virology 263:254-262 (1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20478054; PubMed=11021991;
 RA Sun L., Gurnon J.R., Adams B.J., Graves M.V., Van Etten J.L.;
 RT "Characterization of a beta-1,3-glucanase encoded by chlorella virus
 PBCV-1";
 RL Virology 276:27-36 (2000).
 RN [4]

RP SEQUENCE FROM N.A.
 RA Van Etten J.L.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Van Etten J.L.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Van Etten J.L.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RA Graves M.V., Van Etten J.L.;
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U42580; AAC96463.1;
 SQ SEQUENCE 72 AA; 7701 MW; 300F8BE3D5959C6C CRC64;
 Query Match
 Best Local Similarity 88.2%; Score 30; DB 12; Length 72;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GAFSRAT 7
 Db 36 GAFSRAT 42
 RESULT 4
 ID Q9CVB3 PRELIMINARY; PRT; 164 AA.
 AC Q9CVB3;
 DT 01-JUN-2001 (TRENBLrel. 17. Created)
 DT 01-JUN-2001 (TRENBLrel. 17. Last sequence update)
 DT 01-JUN-2001 (TRENBLrel. 17. Last annotation update)
 DE 2210404M2OR1K protein (Fragment).
 GN 2210404M2OR1K.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CS7BL/6J; TISSUE=STOMACH;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamada I.,
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasuawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Pleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,
 RA Knehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirml L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Baren G.,
 RA Blake J., Boffelli D., Bojunga N., Carimini P., de Bonaldo M.F.,
 RA Brownstein M.J., Bulc C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Holman M., Hume D.A., Kamaya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszynski A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690 (2001).
 DR EMBL; AK008830; BAB25917.1;

GenCore version 5.1.4_P5_4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:56:17 ; Search time 5.55088 Seconds
(without alignments)
168.037 Million cell updates/sec

Title: US-09-644-668A-29

Sequence: 1 GAFSRAT 7

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	34	100.0	7	22	AAB67494	Human light chain
2	31	91.2	112	15	AARS4279	Anti-HIV gp41 immu
3	31	91.2	112	17	AAW01324	Vt of Fab, SS 41 8
4	31	91.2	112	21	AAV95174	Anti-SP41 light ch
5	31	91.2	112	21	AAV98283	Anti-SP41 light ch
6	31	91.2	356	20	AAV34471	Porphyromonas ging
7	31	91.2	491	20	AAV34347	Porphyromonas ging
8	30	88.2	43	22	ABG00976	Novel human diagno
9	29	85.3	46	22	ABG03763	Novel human diagno
10	29	85.3	51	20	AAV41354	Human secreted pro

11	29	85.3	61	22	AA041549	Propionibacterium
12	29	85.3	177	21	AAB51685	Gene 22 human secr
13	29	85.3	177	21	AAB51686	Human secreted pro
14	29	85.3	359	22	AAB30608	Amino acid sequenc
15	29	85.3	373	22	ABG01757	Novel human diagno
16	29	85.3	396	19	AAV56695	Tetracycline resis
17	29	85.3	396	20	AAV42545	Plasmid pRZT1, Te
18	29	85.3	396	20	AAV15383	Plasmid pRZT1, Te
19	29	85.3	396	22	AAB50899	Protein encoded by
20	29	85.3	396	23	AAV75552	cel2 integration v
21	29	85.3	445	21	AAB52291	Bacteriophage coli p
22	29	85.3	1258	21	AAB53204	Macaca mulatta rha
23	29	85.3	85	22	AAV53627	Propionibacterium
24	29	85.3	143	22	AAV56695	Propionibacterium
25	29	85.3	179	22	AAV53900	Propionibacterium
26	29	85.3	259	22	ABG27325	Novel human diagno
27	29	85.3	287	21	AAB35708	Human protein cont
28	29	85.3	361	23	AAB49841	Listeria monocytog
29	29	85.3	410	20	AAW93254	Human ESRP1 protei
30	29	85.3	524	21	AAB58954	Breast and ovarian
31	29	85.3	587	22	AAB74754	Human secreted pro
32	29	85.3	587	23	ABG5328	Human albumin fucl
33	29	85.3	618	22	AAB74769	Human secreted pro
34	29	85.3	675	22	AAW40778	Human polypeptide
35	29	85.3	724	23	ABG04802	LDL receptor bindi
36	29	85.3	791	22	AAE11780	Human kinase (PKIN
37	29	85.3	808	22	AAB65679	Novel protein kina
38	29	85.3	820	21	AAB43354	Human OREF ORF3118
39	29	85.3	832	21	AAB74457	Human TRAF4 bindin
40	29	85.3	924	22	AAW09958	Human cadherin-1 (
41	29	85.3	2139	22	ABG62393	Drosophila melanog
42	29	85.3	27	22	AAW97727	Human peptide #100
43	29	85.3	79.4	18	AAW91383	MEB1 library deriv
44	29	85.3	88	21	AAB40534	Human OREF ORF298
45	29	85.3	95	23	ABP02653	Human OREF protein

ALIGNMENTS

RESULT 1	AA67494	standard; peptide; 7 AA.
XX	AA67494;	
AC	XX	
XX	XX	
DT	29-MAY-2001	(first entry)
XX	XX	
DE	XX	
XX	XX	
KW	Human light chain complementarily determining region 2 (CDR2).	
KW	Complementary determining region; CDR; immune response; antibody;	
KW	cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;	
KW	autoimmune disease; infectious disease; inflammation; allergy;	
KW	rheumatoid arthritis; myasthenia gravis; lupus erythematosus;	
KW	multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;	
KW	transplant rejection; graft versus host disease.	
XX	XX	
OS	Homo sapiens.	
XX	XX	
PN	WO200114424-A2.	
XX	XX	
PD	01-MAR-2001.	
XX	XX	
PP	24-AUG-2000; 2000WO-US23356.	
XX	XX	
PR	24-AUG-1999; 99US-0150452.	
XX	XX	
PA	(MEDA-) MEDAREX INC.	
XX	XX	
PI	Korman AJ, Haik EL, Lonberg N;	
XX	XX	
DR	WPI; 2001-202933/20.	
XX	XX	

14-APR-1994

PN WO9602273-A1

PN WO9602273-A1

GenCore version 5.1.4_P5_4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 17:21:54 ; Search time 2.06316 Seconds
(without alignments)
256.547 Million cell updates/sec

Title: US-09-644-668A-29

Sequence: 1 GARSRA7

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 288829 seqs, 7561385 residues

Number of hits satisfying chosen parameters: 288829

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep:.*
4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep:.*
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12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep:.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep:.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	29	85.3	9	US-10-029-180-138	Sequence 138, App
2	28	82.4	524	US-10-102-806-662	Sequence 662, App
3	28	82.4	924	US-09-838-529-2	Sequence 2, Appl
4	27	79.4	151	US-09-893-737-240	Sequence 240, App
5	27	79.4	427	US-09-975-719-107	Sequence 107, App
6	26	76.5	7	US-09-828-708-45	Sequence 45, Appl
7	26	76.5	7	US-09-828-708-47	Sequence 47, Appl
8	26	76.5	7	US-09-828-708-48	Sequence 48, Appl
9	26	76.5	7	US-09-828-708-49	Sequence 49, Appl
10	26	76.5	72	US-09-796-692-2362	Sequence 2362, Ap
11	26	76.5	74	US-10-125-687-23	Sequence 23, Appl
12	26	76.5	74	US-10-025-687-23	Sequence 23, Appl
13	26	76.5	96	US-10-194-975-82	Sequence 82, Appl
14	26	76.5	104	US-09-828-708-6	Sequence 6, Appl
15	26	76.5	105	US-09-828-708-3	Sequence 3, Appl
16	26	76.5	105	US-09-828-708-5	Sequence 5, Appl
17	26	76.5	105	US-09-828-708-7	Sequence 7, Appl
18	26	76.5	107	US-08-844-215-8	Sequence 8, Appl
19	26	76.5	108	US-09-848-798-178	Sequence 178, App

20	26	76.5	109	9	US-10-125-687-10	Sequence 10, Appl
21	26	76.5	109	12	US-10-025-687-10	Sequence 10, Appl
22	26	76.5	110	9	US-10-001-934-40	Sequence 40, Appl
23	26	76.5	102	10	US-09-815-242-10606	Sequence 10606, A
24	26	76.5	236	10	US-09-859-053-34	Sequence 34, Appl
25	26	76.5	236	10	US-09-859-053-38	Sequence 38, Appl
26	26	76.5	245	9	US-09-880-748-1896	Sequence 1896, Ap
27	26	76.5	246	9	US-09-880-748-1264	Sequence 1264, Ap
28	26	76.5	249	9	US-09-880-748-1035	Sequence 1035, Ap
29	26	76.5	251	10	US-09-880-748-1219	Sequence 1219, Ap
30	26	76.5	251	10	US-09-815-242-12053	Sequence 12053, A
31	26	76.5	253	9	US-09-880-748-1499	Sequence 1499, Ap
32	26	76.5	303	9	US-10-063-547-166	Sequence 166, App
33	26	76.5	303	9	US-10-174-590-562	Sequence 562, App
34	26	76.5	303	9	US-10-176-758-562	Sequence 562, App
35	26	76.5	303	9	US-10-063-516-166	Sequence 166, App
36	26	76.5	303	9	US-10-175-737-562	Sequence 562, App
37	26	76.5	303	9	US-10-063-502-166	Sequence 166, App
38	26	76.5	303	9	US-10-173-706-562	Sequence 562, App
39	26	76.5	303	9	US-10-175-738-562	Sequence 562, App
40	26	76.5	303	9	US-10-175-752-562	Sequence 562, App
41	26	76.5	303	9	US-10-176-482-562	Sequence 562, App
42	26	76.5	303	9	US-10-176-757-562	Sequence 562, App
43	26	76.5	303	9	US-10-176-913-562	Sequence 562, App
44	26	76.5	303	9	US-10-180-552-562	Sequence 562, App
45	26	76.5	303	9	US-10-180-557-562	Sequence 562, App

ALIGNMENTS

RESULT 1
US-10-029-180-138
Sequence 138, Application US/10029180
Publication No. US20020182708A1
GENERAL INFORMATION:
APPLICANT: Calli, Brian M.
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin T.
APPLICANT: Milna, G. Todd
APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeffrey C.
APPLICANT: Trueheart, Josh
APPLICANT: Zhang, Lixin
TITLE OF INVENTION: No. US20020182708A1el Regulators of Fungal Gene Expression
FILE REFERENCE: MIC-004
CURRENT APPLICATION NUMBER: US/10/029,180
CURRENT FILING DATE: 2001-12-22
PRIOR APPLICATION NUMBER: US 60/257,431
PRIOR FILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 138
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 138
LENGTH: 805
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fungal gene
US-10-029-180-138
Query Match 85.3%; Score 29; DB 9; Length 805;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
CY 1 GARSRA7 7
DB 797 GARSRA7 803
RESULT 2
US-10-102-806-662
Sequence 662, Application US/10102806
Publication No. US20030054421A1

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; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: P403P1C1
; CURRENT APPLICATION NUMBER: US/10/102,806
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/0588T
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 662
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (124)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (191)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-102-806-662

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Query Match      82.4%; Score 28; DB 9; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2 AFSRAT 7
Db 422 AFSRAT 427

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RESULT 3
US-09-838-529-2
; Sequence 2, Application US/09838529
; Patent No. US20020081599A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Roy A. J.
; TITLE OF INVENTION: 57809 AND 57798, NOVEL HUMAN CADHERIN
; FILE REFERENCE: MNT-145
; CURRENT APPLICATION NUMBER: US/09/838,529
; CURRENT FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,466
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 2
; LENGTH: 924
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-838-529-2

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Query Match      82.4%; Score 28; DB 10; Length 924;
Best Local Similarity 71.4%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 GAFSRAT 7
Db 33 GAFSRAT 39

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RESULT 4
US-09-893-737-240
; Sequence 240, Application US/09893737
; Patent No. US20020110855A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Presnell, Scott R.

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; TITLE OF INVENTION: MAMMALIAN SECRETED PROTEINS
; FILE REFERENCE: 00-41
; CURRENT APPLICATION NUMBER: US/09/893,737
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 60/215,446
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 240
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-893-737-240

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Query Match      79.4%; Score 27; DB 10; Length 151;
Best Local Similarity 71.4%; Pred. No. 68;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 GAFSRAT 7
Db 142 GAFSRAT 148

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RESULT 5
US-09-975-719-107
; Sequence 107, Application US/09975719
; Publication No. US20030022349A1
; GENERAL INFORMATION:
; APPLICANT: Auebel, Frederick M.
; APPLICANT: Rahme, Laurence G.
; TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
; FILE REFERENCE: 00786/361003
; CURRENT APPLICATION NUMBER: US/09/975,719
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 09/199,637
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: US 60/066,517
; PRIOR FILING DATE: 1997-11-25
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 107
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-975-719-107

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Query Match      79.4%; Score 27; DB 9; Length 427;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 GAFSRAT 7
Db 127 GAFSRAT 133

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RESULT 6
US-09-828-708-45
; Sequence 45, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their parts
; FILE REFERENCE: 1361.005U51
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 45
; LENGTH: 7

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GenCore version 5.1.4_P5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2003, 17:15:40 ; Search time 1.79298 Seconds
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114.870 Million cell updates/sec

Title: US-09-644-668A-29

Sequence: 34

Scoring table: BIOSUM62

Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

To: Number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match Length	DB ID	Description
1	31	91.2	112 1 US-08-276-852-151	Sequence 151, App
2	31	91.2	112 1 US-08-899-575-151	Sequence 151, App
3	31	91.2	112 1 US-08-899-575-151	Sequence 151, App
4	31	91.2	112 5 PCT-US95-08743-151	Sequence 151, App
5	29	85.3	396 2 US-08-850-880-4	Sequence 4, Appl
6	29	85.3	396 2 US-08-944-916-4	Sequence 4, Appl
7	29	85.3	396 2 US-08-814-877-4	Sequence 4, Appl
8	29	85.3	396 4 US-08-272-432A-4	Sequence 4, Appl
9	28	82.4	724 4 US-09-362-737-25	Sequence 25, Appl
10	27	79.4	427 4 US-09-199-637A-107	Sequence 39, Appl
11	26	76.5	56 1 US-08-162-102C-39	Sequence 107, Appl
12	26	76.5	107 1 US-08-107-669D-14	Sequence 14, Appl
13	26	76.5	107 1 US-08-472-788A-14	Sequence 14, Appl
14	26	76.5	107 2 US-08-477-531B-14	Sequence 14, Appl
15	26	76.5	107 2 US-08-652-558-49	Sequence 14, Appl
16	26	76.5	107 2 US-08-082-842A-14	Sequence 14, Appl
17	26	76.5	108 1 US-07-634-278-86	Sequence 14, Appl
18	26	76.5	108 1 US-08-477-728-86	Sequence 86, Appl
19	26	76.5	108 1 US-08-474-040-86	Sequence 86, Appl
20	26	76.5	108 1 US-08-487-200-86	Sequence 86, Appl
21	26	76.5	108 1 US-08-468-113B-150	Sequence 150, App
22	26	76.5	108 1 US-08-477-484B-150	Sequence 150, App
23	26	76.5	108 1 US-08-646-360-150	Sequence 150, App
24	26	76.5	108 2 US-08-232-081B-42	Sequence 42, Appl
25	26	76.5	108 4 US-08-839-765-150	Sequence 150, App
26	26	76.5	108 4 US-09-136-389-150	Sequence 150, App
27	26	76.5	108 4 US-08-484-537-86	Sequence 86, Appl

28	26	76.5	108 4 US-09-240-274-178	Sequence 178, App
29	26	76.5	108 4 US-09-610-838-150	Sequence 150, App
30	26	76.5	109 1 US-08-162-102C-24	Sequence 24, Appl
31	26	76.5	109 4 US-09-025-769B-16	Sequence 16, Appl
32	26	76.5	109 5 PCT-US93-08786-24	Sequence 24, Appl
33	26	76.5	110 4 US-09-025-769B-30	Sequence 30, Appl
34	26	76.5	110 4 US-09-025-769B-47	Sequence 47, Appl
35	26	76.5	116 1 US-08-053-131-183	Sequence 183, App
36	26	76.5	116 2 US-08-096-762-183	Sequence 183, App
37	26	76.5	116 4 US-09-042-353-46	Sequence 46, Appl
38	26	76.5	116 4 US-08-758-417A-311	Sequence 311, App
39	26	76.5	117 1 US-08-466-033-164	Sequence 164, App
40	26	76.5	117 2 US-08-444-733-164	Sequence 164, App
41	26	76.5	117 2 US-08-464-134-164	Sequence 164, App
42	26	76.5	117 2 US-08-461-361-164	Sequence 164, App
43	26	76.5	117 2 US-08-485-910-164	Sequence 164, App
44	26	76.5	129 2 US-08-480-774A-4	Sequence 4, Appl
45	26	76.5	232 1 US-08-638-911A-33	Sequence 33, Appl

ALIGNMENTS

RESULT 1
US-08-276-852-151
Sequence 151, Application US/08276852
Patent No. 5652138

GENERAL INFORMATION:

APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312

INFORMATION FOR SEQ ID NO: 151:

SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-276-852-151

Query Match 91.2% Score 31; DB 1; Length 112;
Best Local Similarity 85.7% Pred. No. 4.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 51 GAYSRA1 57

RESULT 2
US-08-899-575-151
Sequence 151, Application US/08899575
Patent No. 5770440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 151:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-151

Query Match 91.2% Score 31; DB 1; Length 112;
Best Local Similarity 85.7% Pred. No. 4.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 51 GAYSRA1 57

RESULT 3
US-08-899-575-151
Sequence 151, Application US/08899575

Patent No. 5804440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 151:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-151

Query Match 91.2% Score 31; DB 1; Length 112;
Best Local Similarity 85.7% Pred. No. 4.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 51 GAYSRA1 57

RESULT 4
PCT-US95-08743-151
Sequence 151, Application PC/TUS9508743
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08743

GenCore version 5.1.4.p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2003, 17:11:36 / Search time 5.24912 Seconds
(without alignments)
311.344 Million cell updates/sec

Title: US-09-644-668a-32

Sequence: 1 F1SYDGNKRYADSVK 17

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR 73:***
1: p1r1:***
2: p1r2:***
3: p1r3:***
4: p1r4:***

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	83	89.2	98 2 S29543	Ig heavy chain V r
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3	83	89.2	134 2 S31688	Ig heavy chain V r
4	83	89.2	135 2 S31598	Ig heavy chain V r
5	83	89.2	140 2 S70442	Ig heavy chain V r
6	82	88.2	94 2 PL0120	Ig heavy chain V-I
7	82	88.2	97 2 S44115	Ig heavy chain V-I
8	82	88.2	98 2 PL0116	Ig heavy chain V-I
9	82	88.2	98 2 S29544	Ig heavy chain V-I
10	82	88.2	109 2 PH1644	Ig heavy chain V r
11	82	88.2	109 2 PH1646	Ig heavy chain V r
12	82	88.2	111 2 PH1643	Ig heavy chain V r
13	82	88.2	111 2 PH1645	Ig heavy chain V r
14	82	88.2	113 2 S38490	Ig heavy chain V r
15	82	88.2	114 2 S46390	Ig heavy chain V r
16	82	88.2	114 2 S46392	Ig heavy chain V r
17	82	88.2	117 2 S36270	Ig heavy chain V r
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20	82	88.2	119 2 F36005	Ig heavy chain - h
21	82	88.2	120 2 S31112	Ig heavy chain V r
22	82	88.2	121 2 S19666	Ig heavy chain - h
23	82	88.2	121 2 G36005	Ig heavy chain V r
24	82	88.2	122 2 E36005	Ig heavy chain V r
25	82	88.2	122 2 S31119	Ig heavy chain V r
26	82	88.2	123 2 S36493	Ig heavy chain - h
27	82	88.2	130 2 P10098	Ig heavy chain - h
28	82	88.2	132 2 S31603	Ig heavy chain pre
29	82	88.2	134 2 S31679	Ig heavy chain V r

30	82	88.2	139 2 S31674	Ig heavy chain V r
31	78	83.9	76 2 S31592	Ig heavy chain V r
32	78	83.9	133 2 S31510	Ig heavy chain - h
33	77	82.8	122 1 M3H0AM	Ig heavy chain V-I
34	77	82.8	137 2 S31701	Ig heavy chain V r
35	75	80.6	108 2 PH1642	Ig heavy chain V r
36	75	80.6	114 2 S46391	Ig heavy chain V r
37	75	80.6	119 2 PH1660	Ig heavy chain V r
38	75	80.6	118 2 S31117	Ig heavy chain V r
39	75	80.6	122 2 S31111	Ig heavy chain - h
40	75	80.6	128 2 S48791	Ig heavy chain - h
41	75	80.6	133 2 A49028	Ig heavy chain V r
42	74	79.6	110 2 S69897	Ig heavy chain V r
43	74	79.6	118 2 PH1662	Ig heavy chain V r
44	72	77.4	121 2 PH1661	Ig heavy chain V r
45	71	76.3	119 2 S37453	Ig mu chain - huma

ALIGNMENTS

RESULT 1
S29543
Ig heavy chain V region (COS 3) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 07-Jan-1994 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C/Accession: S29543
R/Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.
submitted to the EMBL Data Library, October 1992
A/Reference number: S29543
A/Accession: S29543
A/Molecule type: DNA
A/Residues: 1-98 <NM>
A/Cross-references: EMBL:Z17389; NID:G32835; PIDN:CAA78994.1; PID:G32836
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
C/Keyword: heterotrimer; Immunoglobulin
F/15-98/Domain: Immunoglobulin homology <IMM>

Query Match 89.2%; Score 83; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 9.2e-06;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 F1SYDGNKRYADSVK 17
Db 50 F1RYDGNKRYADSVK 66

RESULT 2

S36259
Ig heavy chain V region (clone alpha-TNF-A1) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C/Accession: S36259
R/Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A/Title: Human anti-self antibodies with high specificity from phage display libraries.
A/Reference number: S36256; MIMD:93178448; PMID:7679990
A/Accession: S36259
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-117 <GR1>
A/Cross-references: EMBL:Z18650; NID:G33123; PIDN:CAA79302.1; PID:G939902
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
C/Keyword: heterotrimer; Immunoglobulin
F/15-98/Domain: Immunoglobulin homology <IMM>

Query Match 89.2%; Score 83; DB 2; Length 117;
Best Local Similarity 88.2%; Pred. No. 1.1e-05;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 F1SYDGNKRYADSVK 17
Db 50 F1RYDGNKRYADSVK 66

RESULT 3

S31688
Ig heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31688
R/CuSinter: A.M.; Gauthier, L.; Boudil, L.; Fougereau, M.; Tonnelie, C.
Submitted to the EMBL Data Library, June 1992
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31585
A/Accession: S31688
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-134 <CUI>
A/Cross-references: EMBL:214174; NID:931013; PIDN:CAA78543.1; PID:931014
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/31-14/Domain: immunoglobulin homology <IMM>

Query Match 89.2%; Score 83; DB 2; Length 134;
Best Local Similarity 88.2%; Pred. No. 1.3e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 F1SYDGNKRYADSVKG 17
|||:|||||
DB 66 F1RYDGSNKRYADSVKG 82

RESULT 4

S31598
Ig heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31598
R/CuSinter: A.M.; Gauthier, L.; Boudil, L.; Fougereau, M.; Tonnelie, C.
Submitted to the EMBL Data Library, June 1992
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31585
A/Accession: S31598
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-135 <CUI>
A/Cross-references: EMBL:214170; NID:931001; PIDN:CAA78539.1; PID:931002
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/31-14/Domain: immunoglobulin homology <IMM>

Query Match 89.2%; Score 83; DB 2; Length 135;
Best Local Similarity 88.2%; Pred. No. 1.3e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 F1SYDGNKRYADSVKG 17
|||:|||||
DB 66 F1RYDGSNKRYADSVKG 82

RESULT 5

S70442
Ig heavy chain precursor V region (mu) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 21-Jan-2000
C/Accession: S70442
R/CuSinter: A.M.; Fumoux, P.; Fougereau, M.; Tonnelie, C.
Mol. Immunol. 29, 1363-1373, 1992
A/Title: IGM kappa/lambda BV human B cell clone: an early step of differentiation of B
A/Reference number: S70442; MUID:93024508; PMID:1383695
A/Accession: S70442
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-140 <CUI>
C/Superfamily: immunoglobulin V region; immunoglobulin homology

F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 89.2%; Score 83; DB 2; Length 140;
Best Local Similarity 88.2%; Pred. No. 1.3e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 F1SYDGNKRYADSVKG 17
|||:|||||
DB 69 F1RYDGSNKRYADSVKG 85

RESULT 6

PL0120
Ig heavy chain V-III region (TD-Vo) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 16-Aug-1996
C/Accession: PL0120
R/Bird, U.; Gallil, N.; Link, M.; Stiles, D.; Sklar, J.
J. Exp. Med. 168, 229-245, 1988
A/Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobu
A/Reference number: PL0116; MUID:88286083; PMID:2840480
A/Accession: PL0120
A/Molecule type: mRNA
A/Residues: 1-94 <BIR>
A/Experimental source: B cells from patient TD with acute lymphoblastic leukemia. ALL
A/Note: the sequence shows the V region (TD-Vo) from a nonproductive DNA rearrangement
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin
F/31-35/Region: complementarity-determining 1
F/49-65/Region: complementarity-determining 2

Query Match 88.2%; Score 82; DB 2; Length 94;
Best Local Similarity 93.8%; Pred. No. 1.3e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISYDGNKRYADSVKG 17
|||:|||||
DB 51 ISYDGSNKRYADSVKG 66

RESULT 7

S44115
Ig heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C/Accession: S44115
R/Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
Submitted to the EMBL Data Library, March 1994
A/Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable
A/Reference number: S44105
A/Accession: S44115
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-97 <HAM>
A/Cross-references: EMBL:231384; NID:9472969; PIDN:CAA83259.1; PID:940526
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 88.2%; Score 82; DB 2; Length 97;
Best Local Similarity 93.8%; Pred. No. 1.3e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISYDGNKRYADSVKG 17
|||:|||||
DB 51 ISYDGSNKRYADSVKG 66

RESULT 8

PL0116
Ig heavy chain V-III region (AW-Vx) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999
C/Accession: PL0116; S26892

1	77	82.8	122	1	HV3G_HUMAN	P01768	homo sapiens
2	67	72.0	122	1	HV3H_HUMAN	P01769	homo sapiens
3	66	71.0	119	1	HV3I_HUMAN	P01770	homo sapiens
4	63	67.7	119	1	HV3L_HUMAN	P01773	homo sapiens
5	57	61.3	116	1	HV05_CARAU	P19181	carassius auratus
6	54	58.1	121	1	HV3B_HUMAN	P01763	homo sapiens
7	54	58.1	121	1	HV3E_HUMAN	P01771	homo sapiens
8	53	57.0	115	1	HV3F_HUMAN	P01771	homo sapiens
9	53	57.0	115	1	HV3G_HUMAN	P01767	homo sapiens
10	52	55.9	119	1	HV3M_HUMAN	P01772	homo sapiens
11	52	55.9	119	1	HV3N_HUMAN	P01774	homo sapiens
12	52	55.9	122	1	HV3A_HUMAN	P01775	homo sapiens
13	50	53.8	117	1	HV3C_HUMAN	P01762	homo sapiens
14	49	52.7	117	1	HV5A_MOUSE	P01764	homo sapiens
15	49	52.7	117	1	HV5B_MOUSE	P18525	mus musculus
16	48	51.6	120	1	HV3J_HUMAN	P18526	mus musculus
17	46.5	50.0	264	1	GUNS_EKPCA	P01782	homo sapiens
18	46	49.5	98	1	HV5I_MOUSE	P16630	erythrina carat
19	45	48.4	117	1	HV5J_MOUSE	P18524	mus musculus
20	45	48.4	120	1	HV3E_HUMAN	P18524	mus musculus
21	44	47.3	97	1	HV5E_MOUSE	P01766	homo sapiens
22	44	47.3	116	1	HV5O_MOUSE	P18527	mus musculus
23	44	47.3	780	1	TREB_YEAST	P18531	mus musculus
24	43	46.2	116	1	HV3T_HUMAN	P35172	saccharomyces
25	43	46.2	117	1	HV03_CARAU	P01781	homo sapiens
26	43	46.2	117	1	HV5S_MOUSE	P19180	carassius auratus
27	43	46.2	367	1	Y046_MYCTU	P18529	mus musculus
28	42	45.2	136	1	HV16_MOUSE	P71013	mycobacterium
29	42	45.2	229	1	Y997_HAEFI	P01783	mus musculus
30	42	45.2	261	1	NUIN_PASTE	P44090	haemophilus
31	42	45.2	360	1	Y06G_ECOLI	P05513	paramecium
32	42	45.2	360	1	Y06G_ECOLI	P53941	escherichia
33	42	45.2	473	1	6P6D_CHIMP	Q92949	buchnera ap
					6P6D_CHIMP	Q92949	chlamydia m

OC Eukaryota; Metazoa; Chordata; Crniata; Vertebrata; Euteleostomi
OC Mammalia; Eutelia; Primates; Carnivora; Homiidae; Homo.
NCBI_TaxId=9606;
(1)
RN SEQUENCE.
RP
MEDLINE=74175307; PubMed=4208843;
RX

RA Florent G., Lehman D., Putnam F.W.;
 RT "The switch point in mu heavy chains of human IgM immunoglobulins."
 RL Biochemistry 13:2482-2498(1974).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
 CC MACROGLOBULIN.
 DR PIR; A02052; M3HGA.
 DR HSSP; P01772; 2FBA.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KM Immunoglobulin V region.
 FT MOD RES 1
 FT NON TER 122
 SQ SEQUENCE 122 AA; 13166 MW; 7455B6959584100A CRC64;
 Query Match 72.0%; Score 67; DB 1; Length 122;
 Best Local Similarity 68.8%; Pred. No. 0.00037;
 Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 Db 51 ISYGBBKYADSVNG 17
 2 ISYDNNKYADSVNG 17
 |||:|||||
 |||:|||||

RESULT 3

HV3L_HUMAN
 ID HV3L_HUMAN STANDARD; PRT; 119 AA.
 AC P01770;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-II region NIE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=77070269; PubMed=826475;
 RA Ponsingl H., Hilschmann N.;
 RT "The rule of antibody structure. The primary structure of a
 RT monoclonal IgG1 immunoglobulin (myeloma protein Nle). III. The
 RT chymotryptic peptides of the H-chain, alignment of the tryptic
 RT peptides and discussion of the complete structure."
 RL Hoppe-seyler's Z. Physiol. Chem. 357:1571-1604(1976).
 RN [2]
 RP DISULFIDE BOND.
 RX MEDLINE=77070267; PubMed=1002129;
 RA Kreker L., Schwarz J., Reichel W., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT IgG1 immunoglobulin (myeloma protein Nle). I: Purification and
 RT characterization of the protein, the L- and H-chains, the
 RT cyanoogen bromide cleavage products, and the disulfide bridges."
 RL Hoppe-seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IG1 MYELOMA
 CC PROTEIN.
 DR PIR; A02053; GIHUNI.
 DR HSSP; P01772; 2FBA.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KM Immunoglobulin V region.
 FT MOD RES 1
 FT NON TER 122
 SQ SEQUENCE 119 AA; 13242 MW; C96935A6555E165B CRC64;

Query Match 71.0%; Score 66; DB 1; Length 119;
 Best Local Similarity 62.5%; Pred. No. 0.00052;
 Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ISYDNNKYADSVNG 17
 :||:|||||
 Db 51 MSYGBBKYADSVNG 66

RESULT 4

HV3L_HUMAN
 ID HV3L_HUMAN STANDARD; PRT; 119 AA.
 AC P01773;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-II region BUR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE (MYELOMA PROTEIN BUR).
 RX MEDLINE=7915106; PubMed=107164;
 RA Putnam F.W., Liu Y.-S.V., Low T.L.K.;
 RT "Primary structure of a human IgM immunoglobulin. IV. Streptococcal
 RT IgM protease, digestion, Fab and Fc fragments, and the complete
 RT amino acid sequence of the alpha 1 heavy chain."
 RL J. Biol. Chem. 254:2865-2874(1979).
 DR PIR; A02056; AIHUBR.
 DR HSSP; P01772; 2FBA.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KM Immunoglobulin V region; Glycoprotein.
 FT MOD RES 1
 FT DISULFID 22
 FT CARBOHYD 28
 FT NON TER 119
 SQ SEQUENCE 119 AA; 12981 MW; 12A709A75344D024 CRC64;
 Query Match 67.7%; Score 63; DB 1; Length 119;
 Best Local Similarity 68.8%; Pred. No. 0.0016;
 Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ISYDNNKYADSVNG 17
 |||:|||||
 Db 51 ISYGBBKYADSVNG 66

RESULT 5

HV05_CARAU
 ID HV05_CARAU STANDARD; PRT; 116 AA.
 AC P19181;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region 5A precursor.
 OS Carassius auratus (Goldfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Carassius.
 NCBI_TaxID=79571;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8814476; PubMed=3125551;
 RA Wilson M.R., Middleton D., Warr G.W.;
 RT "Immunoglobulin heavy chain variable region gene evolution: structure
 RT and family relationships of two genes and a pseudogene in a teleost
 RT fish."
 RL Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).
 DR PIR; B28966; B28966.
 DR HSSP; P01772; 2FBA.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.

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OM protein - protein search, using sw model

Run on: April 16, 2003, 17:13:59 ; Search time 17.4175 Seconds

(Without alignments)
201.108 Million cell updates/sec

Title: US-09-644-668A-32

Sequence: 1 F1SYDGNKRYADSVKG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

To: number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp Vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvitus:*
- 16: sp_bacteriapi:*
- 17: sp_archaeap:*

red. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	89.2	113	4	Q9UL90
2	82	88.2	116	4	Q9UL93
3	82	88.2	613	4	Q8WTK1
4	69	74.2	122	4	Q9UL84
5	65	69.3	147	4	Q9Y509
6	61	65.6	118	4	Q9UL72
7	60	64.5	95	4	Q9UL86
8	54	58.1	121	4	Q9UL71
9	50	53.8	536	5	O45984
10	49	52.7	479	11	Q91WPS
11	48	51.6	71	7	Q9XRR6
12	48	51.6	71	7	Q9GJ71
13	48	51.6	486	11	Q91Z07
14	47	50.5	112	4	Q9HCCI
15	47	50.5	119	11	Q920E7
16					Q920E7 mus musculi

17	47	50.5	2203	5	Q963L8	Q963L8 schistosoma
18	46	49.5	308	2	Q9S0K5	Q9S0K5 shewanella
19	46	49.5	469	2	Q9FAR9	Q9FAR9 shewanella
20	46	49.5	576	13	Q8OHJ1	Q8OHJ1 brachydanio
21	46	49.5	609	12	Q9EMFO	Q9EMFO amaseta moe
22	45	48.4	273	16	Q92FT5	Q92FT5 listeria in
23	45	48.4	273	16	Q8YA04	Q8YA04 listeria mo
24	45	48.4	305	17	Q97CD6	Q97CD6 thermoplasma
25	45	48.4	612	13	Q9DDC6	Q9DDC6 melanogram
26	44	47.3	71	7	Q31366	Q31366 brachydanio
27	44	47.3	87	10	Q9AV03	Q9AV03 oryza sativ
28	44	47.3	175	2	Q9LWC3	Q9LWC3 streptomyces
29	44	47.3	317	5	Q8WR58	Q8WR58 plasmodium
30	44	47.3	326	5	Q8WP98	Q8WP98 plasmodium
31	44	47.3	414	5	Q963G5	Q963G5 plasmodium
32	44	47.3	416	4	Q9NPP6	Q9NPP6 plasmodium
33	44	47.3	491	5	Q963G9	Q963G9 plasmodium
34	44	47.3	574	16	Q9RTW1	Q9RTW1 vibrio chol
35	44	47.3	606	16	Q977Y3	Q977Y3 clostridium
36	44	47.3	683	2	Q914N0	Q914N0 streptococc
37	44	47.3	735	2	Q8VP61	Q8VP61 streptococc
38	44	47.3	785	16	Q980S3	Q980S3 mycoplasma
39	44	47.3	1956	5	Q962L5	Q962L5 plasmodium
40	43	46.2	71	7	Q9XKR9	Q9XKR9 sigmoidon hi
41	43	46.2	71	7	Q9XKR5	Q9XKR5 sigmoidon hi
42	43	46.2	71	7	Q9XKR3	Q9XKR3 sigmoidon hi
43	43	46.2	71	7	Q9GJ03	Q9GJ03 sigmoidon hi
44	43	46.2	118	4	Q9UL91	Q9UL91 homo sapien
45	43	46.2	129	2	Q60111	Q60111 yersinia ps

ALIGNMENTS

RESULT 1

Q9UL90 PRELIMINARY; PRT; 113 AA.

AC Q9UL90;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DIC-2001 (TREMBLrel. 19, Last annotation update)
DE Myosin-reactive Immunoglobulin heavy chain variable region (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
RT Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035024; AAD56260.1; -.
DR HSSP; P01772; 2F84.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; 1g_1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA, 12437 MW, ED57FDD19086D07F CRC64;

Query Match 89.2%; Score 83; DB 4; Length 113;
Best Local Similarity 88.2%; Pred. No. 1.8e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 F1SYDGNKRYADSVKG 17
DB 50 F1SYDGNKRYADSVKG 66

RESULT 2

Q9UL93 PRELIMINARY; PRT; 116 AA.
 AC Q9UL93;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035021; AAD56257.1; -
 DR HSSP; P01772; 2F84.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; 1g; 1.
 DR SMART; SM00406; 1g; 1.
 FT NON_TER 1
 FT 116
 SQ SEQUENCE 116 AA; 12444 MW; 0DA0348154D6061 CRC64;

Query Match 88.2%; Score 82; DB 4; Length 116;
 Best Local Similarity 93.8%; Pred. No. 2.6e-05;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISYDGNKRYADSVKG 17
 DB 50 ISYDGNKRYADSVKG 65

RESULT 3

Q8WUK1 PRELIMINARY; PRT; 613 AA.
 AC Q8WUK1;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Hypothetical 67.3 kDa protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TIGSUB-TONSIL;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC020240; AAH20240.1; -
 DR InterPro; IPR003599; IG_V.
 DR InterPro; IPR003597; IG_C1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; 1g; 5.
 DR SMART; SM00409; 1g; 2.
 DR SMART; SM00407; 1g; 4.
 DR SMART; SM00406; 1g; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
 KW Hypothetical protein.
 SQ SEQUENCE 613 AA; 67396 MW; 60C7F5950671E315 CRC64;

Query Match 88.2%; Score 82; DB 4; Length 613;
 Best Local Similarity 93.8%; Pred. No. 0.00017;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISYDGNKRYADSVKG 17
 DB 70 ISYDGNKRYADSVKG 85

RESULT 4

Q9UL84 PRELIMINARY; PRT; 122 AA.
 AC Q9UL84;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035030; AAD56266.1; -
 DR HSSP; P01772; 2F84.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; 1g; 1.
 DR SMART; SM00406; 1g; 1.
 FT NON_TER 1
 FT 122
 SQ SEQUENCE 122 AA; 13579 MW; 36054D41366545B8 CRC64;

Query Match 74.2%; Score 69; DB 4; Length 122;
 Best Local Similarity 81.2%; Pred. No. 0.003;
 Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISYDGNKRYADSVKG 17
 DB 51 ISYDGNKRYADSVKG 66

RESULT 5

Q9Y509 PRELIMINARY; PRT; 147 AA.
 AC Q9Y509;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE VH3 protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96071149; PubMed=7475288;
 RA Cao J., Vesic R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C., Lichtenstein A.K., Berenson J.R.;
 RT "A CD10-positive subset of malignant cells is identified in multiple myeloma using PCR with patient-specific immunoglobulin gene primers";
 RL Leukemia 9:1948-1953(1995).
 DR EMBL; S80860; AAD14339.1; -
 DR HSSP; P01772; 2F84.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; 1g; 1.

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using SW model

Run on: April 16, 2003, 16:56:17 ; Search time 13.4807 Seconds
(without alignments)

168.037 Million cell updates/sec

Title: US-09-644-668a-32

Sequence: 1 FISTYDGNKRYADSVKVG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Tot Number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SID2/gcgdata/geneseq/genesqp-emb1/AA2002.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	93	100.0	17	22	AAB67491 Human heavy chain
2	93	100.0	118	22	AAB67508 Light chain variab
3	93	100.0	118	22	AAB67513 Heavy chain variab
4	88	94.6	17	21	AAB39830 Anti-IL12 antibo
5	87	93.5	17	22	AAU08361 Antibody heavy cha
6	87	93.5	220	22	AAU08384 Anti-ORGP antibo
7	85	91.4	17	21	AAB39836 Anti-IL12 antibo
8	85	91.4	17	21	AAB39838 Anti-IL12 antibo
9	84	90.3	17	21	AAB39829 Anti-IL12 antibo
10	84	90.3	17	21	AAB39833 Anti-IL12 antibo

11	84	90.3	17	21	AAB39835 Anti-IL12 antibo
12	84	90.3	17	21	AAB39837 Anti-IL12 antibo
13	83	89.2	17	21	AAB39487 Anti-IL12 antibo
14	83	89.2	17	21	AAB39503 Anti-IL12 antibo
15	83	89.2	17	21	AAB39511 Anti-IL12 antibo
16	83	89.2	17	21	AAB39828 Anti-IL12 antibo
17	83	89.2	17	21	AAB39832 Anti-IL12 antibo
18	83	89.2	17	21	AAB39834 Anti-IL12 antibo
19	83	89.2	17	21	AAB39842 Anti-IL12 antibo
20	83	89.2	17	21	AAB39865 Anti-IL12 antibo
21	83	89.2	17	21	AAB39871 Anti-IL12 antibo
22	83	89.2	17	21	AAB39881 Anti-IL12 antibo
23	83	89.2	17	22	AAB67496 Human heavy chain
24	83	89.2	98	21	AAB40123 Anti-IL12 antibo
25	83	89.2	114	21	AAB39499 Anti-IL12 antibo
26	83	89.2	115	21	AAB39507 Anti-IL12 antibo
27	83	89.2	115	21	AAB39515 Anti-IL12 antibo
28	83	89.2	115	21	AAB39517 Anti-IL12 antibo
29	83	89.2	115	21	AAB39519 Anti-IL12 antibo
30	83	89.2	115	21	AAB39521 Anti-IL12 antibo
31	83	89.2	115	21	AAB39523 Anti-IL12 antibo
32	83	89.2	115	21	AAB39525 Anti-IL12 antibo
33	83	89.2	115	21	AAB39527 Anti-IL12 antibo
34	83	89.2	115	21	AAB39529 Anti-IL12 antibo
35	83	89.2	115	21	AAB39531 Anti-IL12 antibo
36	83	89.2	115	21	AAB39533 Anti-IL12 antibo
37	83	89.2	115	21	AAB39535 Anti-IL12 antibo
38	83	89.2	115	21	AAB39537 Anti-IL12 antibo
39	83	89.2	115	21	AAB39539 Anti-IL12 antibo
40	83	89.2	115	21	AAB39541 Anti-IL12 antibo
41	83	89.2	115	21	AAB39543 Anti-IL12 antibo
42	83	89.2	115	21	AAB39545 Anti-IL12 antibo
43	83	89.2	115	21	AAB39547 Anti-IL12 antibo
44	83	89.2	115	21	AAB39549 Anti-IL12 antibo
45	83	89.2	115	21	AAB39549 Anti-IL12 antibo

ALIGNMENTS

RESULT 1	AAB67491	standard; peptide; 17 AA.
ID	AAB67491	
XX	XX	
AC	AAB67491;	
XX	XX	
DT	29-MAY-2001 (first entry)	
XX	XX	
DE	Human heavy chain complementarity determining region 2 (CDR2).	
XX	XX	
KW	Cytoplasmic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;	
KW	autoimmune disease; infectious disease; inflammation; allergy;	
KW	rheumatoid arthritis; myasthenia gravis; lupus erythematosus;	
KW	multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;	
KW	transplant rejection; graft versus host disease.	
XX	XX	
OS	Homo sapiens.	
XX	XX	
PN	WO200114424-A2.	
XX	XX	
PD	01-MAR-2001.	
XX	XX	
PF	24-AUG-2000; 2000WO-US23356.	
XX	XX	
PR	24-AUG-1999; 99US-0150452.	
XX	XX	
PA	(MEDA-) MEDAREX INC.	
XX	XX	
PI	Korman AJ, Halk EL, Lonberg N;	
XX	XX	
DR	WPI; 2001-202933/20.	
XX	XX	

PT Novel human sequence antibody that binds to human cytotoxic T
 PT lymphocyte associated antigen-4, useful for inducing, augmenting or
 PT prolonging immune response to antigen or for suppressing immune
 PT response in patient

PS Claim 30; Page 99; 127pp; English.

CC AAB67490-99 and AAB67501-06 represents complementarity determining
 CC regions (CDRs) of human antibodies. The antibodies specifically bind to
 CC human cytotoxic T lymphocyte associated antigen-4 (CTLA-4). Such
 CC antibodies are used in methods for inducing, augmenting or prolonging
 CC an immune response to an antigen in a patient, where the antibodies
 CC block binding of human CTLA-4 to human B7 ligands. The antibodies are
 CC also useful for treating autoimmune disease in a subject caused or
 CC exacerbated by increased activity of T cells and for treating prostate
 CC cancer, melanoma or epithelial cancer. A polyvalent or polyclonal
 CC antibody preparation comprising two antibodies of the invention are
 CC useful for suppressing an immune response in a patient. They are used for
 CC treating cancer, infectious diseases and promoting beneficial autoimmune
 CC components for the treatment of diseases with inflammatory or allergic
 CC components. The polyvalent or polyclonal preparations are useful for
 CC treating autoimmune diseases such as rheumatoid arthritis, myasthenia
 CC gravis and lupus erythematosus, multiple sclerosis, insulin-dependent
 CC diabetes mellitus, transplant rejection, and inflammation, graft versus
 CC host disease.

CC Sequence 17 AA;

Query Match 100.0%; Score 93; DB 22; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.8e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FISTYDGNKKYADSVKG 17
 DB 1 FISTYDGNKKYADSVKG 17

RESULT 2
 AAB67508
 ID AAB67508 standard; peptide; 118 AA.

AC AAB67508;
 DT 29-MAY-2001 (first entry)

DB Light chain variable region of anti-CTLA-4 antibody 10D1.

XX Complementarity determining region; CDR; immune response; antibody;
 KW cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;
 KW autoimmune disease; infectious disease; inflammation; allergy;
 KW rheumatoid arthritis; myasthenia gravis; lupus erythematosus;
 KW multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;
 KW transplant rejection; graft versus host disease.

XX Homo sapiens.

PH Key Location/Qualifiers

FT Region 31..35 /note= "CDR1"
 FT Region 50..66 /note= "CDR2"
 FT Region 99..107 /note= "CDR3"

XX WO200114424-A2.

PD 01-MAR-2001.

XX 24-AUG-2000; 2000WO-US23356.

XX 24-AUG-1999; 99US-0150452.

XX (MEDA-) MEDAREX INC.

XX Korman AJ, Halk EL, Lomborg N;
 DR WPI; 2001-202933/20.

PT Novel human sequence antibody that binds to human cytotoxic T
 PT lymphocyte associated antigen-4, useful for inducing, augmenting or
 PT prolonging immune response to antigen or for suppressing immune
 PT response in patient

PS Claim 25; Fig 7; 127pp; English.

CC The present sequence represents the light chain variable region of
 CC human antibody 10D1. This antibody specifically binds to human
 CC cytotoxic T lymphocyte associated antigen-4 (CTLA-4). Such antibodies
 CC are used in methods for inducing, augmenting or prolonging an immune
 CC response to an antigen in a patient, where the antibodies block
 CC binding of human CTLA-4 to human B7 ligands. The antibodies are
 CC also useful for treating autoimmune disease in a subject caused or
 CC exacerbated by increased activity of T cells and for treating prostate
 CC cancer, melanoma or epithelial cancer. A polyvalent or polyclonal
 CC antibody preparation comprising two antibodies of the invention are
 CC useful for suppressing an immune response in a patient. They are used for
 CC treating cancer, infectious diseases and promoting beneficial autoimmune
 CC components for the treatment of diseases with inflammatory or allergic
 CC components. The polyvalent or polyclonal preparations are useful for
 CC treating autoimmune diseases such as rheumatoid arthritis, myasthenia
 CC gravis and lupus erythematosus, multiple sclerosis, insulin-dependent
 CC diabetes mellitus, transplant rejection, and inflammation, graft versus
 CC host disease.

CC Sequence 118 AA;

Query Match 100.0%; Score 93; DB 22; Length 118;
 Best Local Similarity 100.0%; Pred. No. 4.3e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FISTYDGNKKYADSVKG 17
 DB 50 FISTYDGNKKYADSVKG 66

RESULT 3
 AAB67513
 ID AAB67513 standard; peptide; 118 AA.

AC AAB67513;

DT 29-MAY-2001 (first entry)

DB Heavy chain variable region of anti-CTLA-4 antibody 10D1.

XX Complementarity determining region; CDR; immune response; antibody;
 KW cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;
 KW autoimmune disease; infectious disease; inflammation; allergy;
 KW rheumatoid arthritis; myasthenia gravis; lupus erythematosus;
 KW multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;
 KW transplant rejection; graft versus host disease.

XX Homo sapiens.

PH Key Location/Qualifiers

FT Region 31..35 /note= "CDR1"
 FT Region 50..66 /note= "CDR2"
 FT Region 99..107 /note= "CDR3"

XX WO200114424-A2.

PD 01-MAR-2001.

PF 24-AUG-2000; 2000WO-US23356.
 XX
 PR 24-AUG-1999; 99US-0150452.
 XX
 PA (MEDA-) MEDAREX INC.
 XX
 PI Korman AJ, Halk EL, Longberg N;
 XX
 DR WPI; 2001-202933/20.
 XX
 PT Novel human sequence antibody that binds to human cytotoxic T
 PT lymphocyte associated antigen-4, useful for inducing, augmenting or
 PT prolonging immune response to antigen or for suppressing immune
 XX response in patient
 XX
 PS Claim 25; Fig 8; 127pp; English.
 XX
 CC The present sequence represents the heavy chain variable region of
 CC human antibody 1001. This antibody specifically binds to human
 CC cytotoxic T lymphocyte associated antigen-4 (CTLA-4). Such antibodies
 CC are used in methods for inducing, augmenting or prolonging an immune
 CC response to an antigen in a patient, where the antibodies block
 CC binding of human CTLA-4 to human B7 ligands. The antibodies are
 CC also useful for treating autoimmune disease in a subject caused or
 CC exacerbated by increased activity of T cells and for treating prostate
 CC cancer, melanoma or epithelial cancer. A polyvalent or polyclonal
 CC antibody preparation comprising two antibodies of the invention are
 CC useful for suppressing an immune response in a patient. They are used for
 CC treating cancer, infectious diseases and promoting beneficial autoimmune
 CC reactions for the treatment of diseases with inflammatory or allergic
 CC components. The polyvalent or polyclonal preparations are useful for
 CC treating autoimmune diseases such as rheumatoid arthritis, myasthenia
 CC gravis and lupus erythematosus, multiple sclerosis, insulin-dependent
 CC diabetes mellitus, transplant rejection, and inflammation, graft versus
 CC host disease.
 CC
 SQ Sequence 118 AA;
 XX
 QY 1 FISYDGNKKYYADSVKG 17
 DB 50 FISYDGNKKYYADSVKG 66
 XX
 RESULT 4
 AA 10
 ID AB39830 standard; Peptide; 17 AA.
 AC AAB39830;
 XX
 DT 05-FEB-2001 (first entry)
 XX
 DE Anti-hil-12 antibody heavy chain CDR2 amino acid sequence SEQ ID 346.
 XX
 KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
 KW complementarity determining region; CDR; antihumetic; antiarthritic;
 KW antileukemic; neuroprotective; antiproliferative; antisclerotic; cardiac;
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 PN WO200056772-A1.
 XX
 PD 28-SEP-2000.
 XX
 PF 24-MAR-2000; 2000WO-US07946.
 XX
 PR 25-MAR-1999; 99US-0126603.
 XX

PA (BADI) BASF AG.
 PA (GEM) GENETICS INST INC.
 XX
 PI Salfeld JG, Roguska M, Paekind M, Banerjee S, Tracey DE, White M,
 PI Karmakchalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A, A
 PI Veldman GM, Venturini A, Warner NM, Midom A, Elyan JG, Duncan AR,
 PI Derbyshire EJ, Carmen S, Smith S, Holter TL, Du Fou SJ,
 XX
 DR WPI; 2000-638250/61.
 XX
 PT New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis -
 XX
 XX
 PS Claim 33; Figure 2B; 377pp; English.
 XX
 CC This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 CC anti-IL-12 antibody heavy and light chain complementarity determining
 CC region (CDR) amino acid sequences, and also include variable region
 CC amino acid sequences. Other variable region amino acid sequences are
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
 CC represent anti-IL-12 CDR3 related amino acid sequences. AAB39772-B40063
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 CC given in AAB40064-B40067. Primers used in the identification and
 CC construction of the antibodies of the invention are given in
 CC AAC61062-C61071. The antibody of the invention is a neutralising
 CC antibody and has antirheumatic; antiarthritic; antileukemic;
 CC antiinflammatory; neuroprotective; antiproliferative; antisclerotic;
 CC cardiac; antiparasitic; antibacterial and immunosuppressive activity.
 CC The antibodies or antigen-binding fragments are useful in the treatment
 CC of disorders associated with detrimental release of human IL-12,
 CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
 CC They can also be used in the manufacture of a pharmaceutical composition
 CC to treat human IL-12 disorders.
 CC
 SQ Sequence 17 AA;
 XX
 QY 1 FISYDGNKKYYADSVKG 17
 DB 1 FISYDGNKKYYADSVKG 17
 XX
 RESULT 5
 AAU08361
 ID AAU08361 standard; peptide; 17 AA.
 AC AAU08361;
 XX
 DT 17-DEC-2001 (first entry)
 XX
 DE Antibody heavy chain variable region CDR2 #2.
 XX
 KW Antibody; heavy chain; CDR2; complementarity determining region; Oepdp;
 KW osteoparatic; osteoprotegerin binding protein; osteoclast formation;
 KW bone resorption; loss of bone mass; bone tumour; osteoporosis;
 KW bone cancer; rheumatoid arthritis; hypercalcaemia of malignancy;
 KW steroid-induced osteoporosis.
 XX
 OS Synthetic.
 XX
 PN WO200162932-A1.
 XX
 PD 30-AUG-2001.
 XX
 PF 23-FEB-2001; 2001WO-US05973.
 XX
 PR 23-FEB-2000; 2000US-0511139.
 XX

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 17:21:54 ; Search time 5.01053 Seconds
(Without alignments)
256.547 Million cell updates/sec

Title: US-09-644-668a-32

Sequence: 1 F1SYDGNKRYADSVK 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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To: number of hits satisfying chosen parameters: 288829

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	89.2	249	9	US-09-880-748-1956 Sequence 1956, App
2	83	89.2	251	9	US-09-880-748-952 Sequence 952, App
3	83	89.2	251	9	US-09-880-748-952 Sequence 982, App
4	82	88.2	83	9	US-10-078-958-7 Sequence 7, App1
5	82	88.2	98	9	US-10-194-975-23 Sequence 23, App1
6	82	88.2	98	9	US-10-194-975-24 Sequence 24, App1
7	82	88.2	98	9	US-10-194-975-25 Sequence 25, App1
8	82	88.2	122	9	US-09-144-886-68 Sequence 68, App1
9	82	88.2	122	9	US-09-144-886-69 Sequence 69, App1
10	82	88.2	128	10	US-09-850-165-104 Sequence 104, App
11	82	88.2	238	9	US-09-880-748-1931 Sequence 1931, App
12	82	88.2	241	9	US-09-880-748-2055 Sequence 2055, App
13	82	88.2	247	9	US-09-880-748-924 Sequence 924, App
14	82	88.2	247	9	US-09-880-748-1330 Sequence 1330, App
15	82	88.2	248	9	US-09-880-748-1421 Sequence 1421, App
16	82	88.2	249	9	US-09-880-748-5 Sequence 5, App1
17	82	88.2	249	9	US-09-880-748-397 Sequence 397, App
18	82	88.2	249	9	US-09-880-748-512 Sequence 512, App
19	82	88.2	249	9	US-09-880-748-892 Sequence 892, App

20	82	88.2	249	9	US-09-880-748-911 Sequence 911, App
21	82	88.2	249	9	US-09-880-748-1102 Sequence 1102, App
22	82	88.2	249	9	US-09-880-748-1105 Sequence 1105, App
23	82	88.2	249	9	US-09-880-748-1108 Sequence 1108, App
24	82	88.2	249	9	US-09-880-748-1110 Sequence 1110, App
25	82	88.2	249	9	US-09-880-748-1111 Sequence 1111, App
26	82	88.2	249	9	US-09-880-748-1113 Sequence 1113, App
27	82	88.2	249	9	US-09-880-748-1115 Sequence 1115, App
28	82	88.2	249	9	US-09-880-748-1117 Sequence 1117, App
29	82	88.2	249	9	US-09-880-748-1119 Sequence 1119, App
30	82	88.2	249	9	US-09-880-748-1174 Sequence 1724, App
31	82	88.2	249	9	US-09-880-748-1175 Sequence 1725, App
32	82	88.2	252	9	US-09-880-748-1201 Sequence 1201, App
33	82	88.2	252	9	US-09-880-748-1394 Sequence 1394, App
34	82	88.2	252	9	US-09-880-748-1519 Sequence 1519, App
35	82	88.2	252	9	US-09-880-748-1627 Sequence 1627, App
36	82	88.2	252	9	US-09-880-748-1731 Sequence 1731, App
37	82	88.2	254	9	US-09-880-748-977 Sequence 977, App
38	82	88.2	254	9	US-09-880-748-981 Sequence 981, App
39	82	88.2	254	9	US-09-880-748-983 Sequence 983, App
40	82	88.2	256	9	US-09-880-748-839 Sequence 839, App
41	81	87.1	17	10	US-09-828-708-24 Sequence 24, App1
42	81	87.1	101	10	US-09-828-708-10 Sequence 10, App1
43	81	87.1	241	9	US-09-880-748-1887 Sequence 1887, App
44	81	87.1	241	9	US-09-880-748-1901 Sequence 1901, App
45	81	87.1	243	9	US-09-880-748-1935 Sequence 1935, App

ALIGNMENTS

RESULT 1
US-09-880-748-1956
Sequence 1956, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunoselectively Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1956
LENGTH: 249
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1956

Query Match 89.2% Score 83, DB 9, Length 249;
Best Local Similarity 88.2% Pred. No. 5.9e-05;
Matches 15, Conservative 2, Mismatches 0, Indels 0, Gaps 0;

QY 1 F1SYDGNKRYADSVK 17
|||:|||||
Db 50 F1SYDGNKRYADSVK 66

RESULT 2
US-09-880-748-952
Sequence 952, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:

APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3339
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 952
LENGTH: 251
PE: PRT
ORGANISM: Homo sapiens
US-09-880-748-952

Query Match 89.2%; Score 83; DB 9; Length 251;
Best Local Similarity 88.2%; Pred. No. 5.9e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FSYDGNKRYADSVKG 17
DB 50 FRYDGSNKRYADSVKG 66

RESULT 3
US-09-880-748-982
Sequence 982, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 982
LENGTH: 251
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-982

Query Match 89.2%; Score 83; DB 9; Length 251;
Best Local Similarity 88.2%; Pred. No. 5.9e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FSYDGNKRYADSVKG 17
DB 50 FRYDGSNKRYADSVKG 66
RESULT 4
US-10-078-958-7
Sequence 7, Application US/10078958
Publication No. US20030070185A1

GENERAL INFORMATION:
APPLICANT: JAKOBOVITS, AYA
APPLICANT: KUCHERLAPATI, RAJU
APPLICANT: KLAPHOLZ, SUSAN
APPLICANT: MENDEZ, MICHAEL J.
APPLICANT: GREEN, LARRY
TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN Ig LOCI INCLUDING PLURAL VH AND VK REGIONS AND ANTIBODIES PRODUCED THEREFROM
FILE REFERENCE: CELL 4.18 CON
CURRENT APPLICATION NUMBER: US/10/078,958
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 08/759,620
PRIOR FILING DATE: 1996-12-03
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 83
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD RES
LOCATION: (22)
OTHER INFORMATION: Variable amino acid
US-10-078-958-7

Query Match 88.2%; Score 82; DB 9; Length 83;
Best Local Similarity 93.8%; Pred. No. 2.9e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISYDGNKRYADSVKG 17
DB 36 ISYDGSNKRYADSVKG 51

RESULT 5
US-10-194-975-23
Sequence 23, Application US/10194975
Publication No. US20030039649A1
GENERAL INFORMATION:
APPLICANT: Foote, Jefferson
TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501231.01
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PatentIn version 3.1
SEQ ID NO 23
LENGTH: 98
TYPE: PRT
ORGANISM: Homo sapiens
US-10-194-975-23

Query Match 88.2%; Score 82; DB 9; Length 98;
Best Local Similarity 93.8%; Pred. No. 3.3e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISYDGNKRYADSVKG 17
DB 51 ISYDGSNKRYADSVKG 66

RESULT 6
US-10-194-975-24
Sequence 24, Application US/10194975
Publication No. US20030039649A1
GENERAL INFORMATION:
APPLICANT: Foote, Jefferson
TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501231.01
CURRENT APPLICATION NUMBER: US/10/194,975

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 17:15:40 ; Search time 4.35439 Seconds

(without alignments)
114.870 Million cell updates/sec

Title: US-09-644-668a-32

Perfect score: 93

Sequence: 1 FISTYGNKKYADSVKXG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/6CTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	82	88.2	98	1	US-08-211-202-118 Sequence 118, App
2	82	88.2	116	1	US-08-211-202-141 Sequence 141, App
	82	88.2	117	3	US-08-545-808A-115 Sequence 115, App
	82	88.2	119	1	US-08-331-398A-46 Sequence 46, App
5	82	88.2	119	2	US-08-331-397B-46 Sequence 46, App
6	82	88.2	119	2	US-08-759-804A-46 Sequence 46, App
7	82	88.2	119	4	US-09-227-693-46 Sequence 46, App
8	82	88.2	120	1	US-08-211-202-135 Sequence 135, App
9	82	88.2	120	1	US-07-942-243-35 Sequence 35, App
10	82	88.2	123	4	US-08-983-607-38 Sequence 38, App
11	82	88.2	128	1	US-08-478-039-96 Sequence 96, App
12	82	88.2	128	1	US-08-476-349A-96 Sequence 96, App
13	82	88.2	124	4	US-09-240-274-5 Sequence 5, App
14	82	88.2	124	4	US-09-240-274-6 Sequence 6, App
15	82	88.2	125	1	US-08-276-852-72 Sequence 72, App
16	82	88.2	125	1	US-08-276-852-73 Sequence 73, App
17	82	88.2	125	1	US-08-276-852-74 Sequence 74, App
18	82	88.2	125	1	US-08-276-852-75 Sequence 75, App
19	82	88.2	125	1	US-08-276-852-76 Sequence 76, App
20	82	88.2	125	1	US-08-276-852-77 Sequence 77, App
21	82	88.2	125	1	US-08-899-575-72 Sequence 72, App
22	82	88.2	125	1	US-08-899-575-73 Sequence 73, App
23	82	88.2	125	1	US-08-899-575-74 Sequence 74, App
24	82	88.2	125	1	US-08-899-575-75 Sequence 75, App
25	82	88.2	125	1	US-08-899-575-76 Sequence 76, App
26	82	88.2	125	1	US-08-899-575-77 Sequence 77, App
27	82	88.2	125	1	US-08-899-575-77 Sequence 72, App

28	77	82.8	125	1	US-08-899-575-73 Sequence 73, App
29	77	82.8	125	1	US-08-899-575-74 Sequence 74, App
30	77	82.8	125	1	US-08-899-575-75 Sequence 75, App
31	77	82.8	125	1	US-08-899-575-76 Sequence 76, App
32	77	82.8	125	1	US-08-899-575-77 Sequence 77, App
33	77	82.8	125	5	PCT-US95-08743-72 Sequence 72, App
34	77	82.8	125	5	PCT-US95-08743-73 Sequence 73, App
35	77	82.8	125	5	PCT-US95-08743-74 Sequence 74, App
36	77	82.8	125	5	PCT-US95-08743-75 Sequence 75, App
37	77	82.8	125	5	PCT-US95-08743-76 Sequence 76, App
38	77	82.8	125	5	PCT-US95-08743-77 Sequence 77, App
39	77	82.8	126	4	US-09-240-274-16 Sequence 16, App
40	77	82.8	126	4	US-09-240-274-152 Sequence 152, App
41	77	82.8	127	4	US-09-240-274-139 Sequence 139, App
42	77	82.8	141	1	US-08-259-372A-2 Sequence 2, App
43	77	82.8	141	1	US-08-468-671-2 Sequence 2, App
44	76	81.7	179	4	US-08-862-124-2 Sequence 2, App
45	76	81.7	287	4	US-08-862-124-17 Sequence 17, App

ALIGNMENTS

RESULT 1
US-08-211-202-118
Sequence 118, Application US/08211202
Patent No. 5565332
GENERAL INFORMATION:
APPLICANT: HOOGENBOOM, Hendricus Reneus Jacobus Matheus
APPLICANT: BAIER, Michael
APPLICANT: JESPER, Laurence Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies - a
TITLE OF INVENTION: combinatorial approach
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSER: David W. Clough, Marshall O'Toole Gerstein Murray &
ADDRESSER: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (ERO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,202
FILING DATE: 23-SEP-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120252.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300

TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 118:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-211-202-141

Query Match 88.2%; Score 82; DB 1; Length 98;
Best Local Similarity 93.8%; Pred. No. 4.7e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISYDGNKRYADSVKG 17
DB 51 ISYDGNKRYADSVKG 66

RE 2

US 211-202-141
Sequence 141, Application US/08211202
Patent No. 5565332

GENERAL INFORMATION:
APPLICANT: HOOGENBOOM, Hendricus Renetus Jacobus Matheus
APPLICANT: BAIR, Michael
APPLICANT: JESPER, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies - a
TITLE OF INVENTION: combinatorial approach
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,202
FILING DATE: 23-SEP-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120252.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00863
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 141:
SEQUENCE CHARACTERISTICS:

LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-211-202-141

Query Match 88.2%; Score 82; DB 3; Length 116;
Best Local Similarity 93.8%; Pred. No. 5.6e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISYDGNKRYADSVKG 17
DB 51 ISYDGNKRYADSVKG 66

RESULT 3

US-08-545-809A-115
Sequence 115, Application US/08545809A
Patent No. 6096878

GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 115:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-545-809A-115

Query Match 88.2%; Score 82; DB 3; Length 117;
Best Local Similarity 93.8%; Pred. No. 5.7e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISYDGNKRYADSVKG 17
DB 70 ISYDGNKRYADSVKG 85.

RESULT 4

US-08-331-398A-46
Sequence 46, Application US/08331398A
Patent No. 5608039
GENERAL INFORMATION:

GenCore version 5.1.4.D5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2003, 17:11:36 Search time 2.77895 Seconds
(without alignments)
311.344 Million cell updates/sec

Title: US-09-644-668A-35

Perfect score: 54

Sequence: 1 QOYGSSPWT 9

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Tot number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR 73:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	108	2 C30608	Ig kappa chain V-I
2	54	100.0	129	1 K3H0H1	Ig kappa chain pre
3	51	94.4	118	2 T03036	Ig light chain - h
4	45	83.3	91	2 S67940	Ig kappa chain V-I
5	45	83.3	92	2 S37513	Ig kappa chain V-I
6	45	83.3	109	2 A30608	Ig kappa chain V-I
7	45	83.3	109	2 H30601	Ig kappa chain V-I
8	44	81.5	92	2 S37524	Ig kappa chain V-I
9	44	81.5	108	1 K3H0B6	Ig kappa chain V-I
10	44	81.5	109	2 G30607	Ig kappa chain V-I
11	43.5	80.6	93	2 S37526	Ig kappa chain V-I
12	43	79.6	88	2 PL0261	Ig kappa chain V-I
13	43	79.6	106	2 PL0260	Ig kappa chain V-I
14	43	79.6	130	1 KVM5M4	Ig kappa chain pre
15	42	77.8	92	2 S37533	Ig kappa chain V-I
16	42	77.8	96	2 G38601	Ig kappa chain V-I
17	42	77.8	125	2 S40333	Ig kappa chain V-I
18	42	77.8	126	2 A49137	Ig kappa chain V-I
19	41	75.9	92	2 S37510	Ig kappa chain V-I
20	41	75.9	102	2 A34153	Ig kappa chain V-I
21	41	75.9	108	2 B30608	Ig kappa chain V-I
22	41	75.9	109	1 K3H0S1	Ig kappa chain V-I
23	41	75.9	109	2 B30601	Ig kappa chain V-I
24	41	75.9	109	2 C30601	Ig kappa chain V-I
25	41	75.9	129	2 S49532	Ig kappa chain V-I
26	41	75.9	215	2 A23746	anti-1.5m antibody V
27	41	75.9	391	2 T40029	Ig kappa chain V-I
28	40	74.1	92	2 S37519	hypothetical prote
29	40	74.1	92	2 S37517	Ig kappa chain V-I

30	40	74.1	97	2 PH1085	Ig light chain V-I
31	40	74.1	100	2 S29590	Ig kappa chain V-I
32	40	74.1	106	2 PL0259	Ig kappa chain V-I
33	40	74.1	109	1 K3H0T1	Ig kappa chain V-I
34	40	74.1	109	2 C30601	Ig kappa chain V-I
35	40	74.1	109	2 D30601	Ig kappa chain V-I
36	40	74.1	109	2 F44151	Ig kappa chain V-I
37	40	74.1	109	2 S47181	Ig kappa chain V-I
38	40	74.1	121	2 S40327	Ig kappa chain - h
39	40	74.1	127	2 S04577	Ig kappa chain pre
40	40	74.1	215	2 H85580	hypothetical prote
41	40	74.1	261	1 Q8BPL	recombination prot
42	40	74.1	261	2 G90775	recombination prot
43	40	74.1	261	2 A98004	recombination prot
44	40	74.1	261	2 E85848	hypothetical prote
45	40	74.1	261	2 H85637	recombination prot

ALIGNMENTS

RESULT 1
C30608
Ig kappa chain V-III region (Ple) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 29-Jun-1989 #sequence_rev18101 29-Jun-1989 #text_change 21-Jan-2000
C/Accession: C30608
R/Goni: F.R.; Chen, P.P.; McGinnis, D.; Arjona, M.L.; Fernandez, J.; Carson, D.; Solc
J. Immunol. 142, 3158-3163, 1989
A/Title: Structural and idiotypic characterization of the L chains of human IGM autoanti
A/Reference number: A30601; PMID:89215279; PMID:2496160
A/Accession: C30608
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-108 <GON>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/46-91/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 54; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.02; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QOYGSSPWT 9
Db 90 QOYGSSPWT 98

RESULT 2

K3H0H1
Ig kappa chain precursor V-III region (Hic) - human
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1990 #sequence_rev18101 30-Jun-1990 #text_change 21-Jan-2000
C/Accession: PL0021
R/Klips: T.J.; Tomhave, E.; Chen, P.P.; Carson, D.A.
J. Exp. Med. 167, 840-852, 1988
A/Title: Autoantibody-associated kappa light chain variable region gene expressed in chr
A/Reference number: PL0021; PMID:8811307; PMID:3127527
A/Accession: PL0021
A/Molecule type: mRNA
A/Residues: 1-129 <RIP>
C/Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed 1
C/Genetics:
A/Gene: GDB:IGKV3
A/Cross-references: GDB:136266
A/Map position: 2p12-2p11
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as Iga and IgM, the subunits associate into la
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin
F/1-20/Domain: signal sequence #status predicted <SIG>
F/21-129/Product: Ig kappa chain V-III region (Hic) #status predicted <MAT>
F/21-117/Region: V segment

F/36-111/Domain: immunoglobulin homology <IMM>
 F/44-55/Region: complementarity-determining 1
 F/71-77/Region: complementarity-determining 2
 F/110-117/Region: complementarity-determining 3
 F/118-129/Region: J segment (Jk1)
 F/43-109/Distal/Id bonds: #status predicted

Query Match 100.0%; Score 54; DB 1; Length 129;
 Best Local Similarity 100.0%; Pred. No. 0.024;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOYSSPWT 9
 Db 110 QOYSSPWT 118

RESULT 3
 T03036
 Ig kappa chain - human (fragment)

C/Species: Homo sapiens (man)
 C/Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
 C/Accession: T03036
 R/Van Es, J.H.; Gmelig Meyling, F.H.J.; Vaf de Akker, W.R.M.; Aanstoot, H.; Derksen, R.H.
 J. Exp. Med. 173, 461-470, 1991
 A/Title: Somatic mutations in the variable regions of a human Igg anti-double-stranded D
 A/Reference number: D0428; MUID:91108344; PMID:1899104
 A/Accession: T03036
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-118 <VAN>
 A/Cross-references: EMBL:X56594; NID:936657; PIDN:CAA39932.1; PID:91335324
 A/Experimental source: B-cell
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 F/20-95/Domain: immunoglobulin homology <IMM>

Query Match 94.4%; Score 51; DB 2; Length 118;
 Best Local Similarity 86.9%; Pred. No. 0.072;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOYSSPWT 9
 Db 94 QOYSSPWT 102

RESULT 4
 S67940

Ig kappa chain V region, subgroup III (clone MH52) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 20-Mar-1998
 C/Accession: S67940
 R/Hehman, J.M.; Furmaniak, J.; Pegg, C.; Burton, D.R.; Smith, B.R.
 Autoimmunity 12, 135-141, 1992
 A/Title: Cloning of a human autoimmune response: preparation and sequencing of a human
 A/Reference number: S67940; MUID:92314301; PMID:1617110
 A/Accession: S67940
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-91 <HEX>
 C/Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 83.3%; Score 45; DB 2; Length 91;
 Best Local Similarity 86.9%; Pred. No. 0.61;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOYSSPWT 9
 Db 71 QOYSSPWT 79

RESULT 5
 S37513
 Ig kappa chain V region (V-kappa 3) - human (fragment)

C/Species: Homo sapiens (man)
 C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
 C/Accession: S37513
 R/Klein, U.; Kiepers, R.; Rajewsky, K.
 submitted to the EMBL Data Library, September 1993
 A/Description: Human IGM(+)19D(+) cells, the major B cell subset in the peripheral bl

A/Reference number: S37501
 A/Accession: S37513
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-92 <KLE>
 A/Cross-references: EMBL:Z26598; NID:9405668; PIDN:CAA81352.1; PID:9405669
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin

Query Match 83.3%; Score 45; DB 2; Length 92;
 Best Local Similarity 88.9%; Pred. No. 0.61;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOYSSPWT 9
 Db 73 QOYSSPWT 81

RESULT 6
 A30608

Ig kappa chain V-III region (Son) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
 C/Accession: A30608
 R/Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sc
 J. Immunol. 142, 3158-3163, 1989
 A/Title: Structural and idiotypic characterization of the L chains of human IGM autoar
 A/Reference number: A30601; MUID:89215279; PMID:2496160
 A/Accession: A30608
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-109 <GON>
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F/16-91/Domain: immunoglobulin homology <IMM>

Query Match 83.3%; Score 45; DB 2; Length 109;
 Best Local Similarity 88.9%; Pred. No. 0.73;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOYSSPWT 9
 Db 90 QOYSSPWT 98

RESULT 7
 H30601

Ig kappa chain V-III region (Gar and Flo) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
 C/Accession: H30601; E30601
 R/Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; So
 J. Immunol. 142, 3158-3163, 1989
 A/Title: Structural and idiotypic characterization of the L chains of human IGM autoar
 A/Reference number: A30601; MUID:89215279; PMID:2496160
 A/Accession: H30601
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-109 <GON>
 A/Accession: E30601
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-109 <GON>
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F/16-91/Domain: immunoglobulin homology <IMM>

GenCore version 5.1.4_P5_4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:57:42 Search time 1.76842 Seconds
(without alignment)

211.085 Million cell updates/sec

Title: US-09-644-668A-35

Perfect score: 54

Sequence: 1 QOYSSPWT 9

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

To: number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	129	1	KV3M_HUMAN
2	44	81.5	108	1	KV3A_HUMAN
3	43	79.6	130	1	KV5G_MOUSE
4	41	75.9	109	1	KV3B_HUMAN
5	40	74.1	109	1	KV3D_HUMAN
6	40	74.1	261	1	VBET_LABED
7	39	72.2	367	1	VE2_HPV17
8	39	72.2	377	1	VE2_RCPV1
9	39	72.2	461	1	FUCO_DICDI
10	38	70.4	109	1	KV3G_HUMAN
11	38	70.4	497	1	VE2_HPV20
12	37	68.5	108	1	KV1R_HUMAN
13	37	68.5	129	1	VE2_HPV4
14	37	68.5	377	1	VE2_HPV4
15	37	68.5	463	1	VE2_HPV4
16	37	68.5	1066	1	HYSA_STRPN
17	36	66.7	128	1	KV3K_HUMAN
18	36	66.7	134	1	KV4C_HUMAN
19	36	66.7	382	1	VE2_HPV5
20	36	66.7	388	1	VE2_HPV29
21	36	66.7	388	1	VE2_HPV50
22	36	66.7	388	1	VE2_HPV42
23	36	66.7	452	1	VE2_HPV17
24	36	66.7	461	1	VE2_HPV09
25	35	64.8	108	1	KV1B_HUMAN
26	35	64.8	227	1	ID11_SCHPO
27	35	64.8	378	1	VE2_HPV5
28	35	64.8	436	1	VE2_HPV22
29	35	64.8	493	1	VE2_HPV19
30	35	64.8	2483	1	COA2_HUMAN
31	34.5	63.9	479	1	PAX3_HUMAN
32	34.5	63.9	479	1	PAX3_MOUSE
33	34	63.0	218	1	Y522_HABIN

34	34	63.0	254	1	HM36_CABEL
35	34	63.0	288	1	CYST_MARPO
36	34	63.0	493	1	PCD_ARTOX
37	34	63.0	575	1	I10R_MOUSE
38	34	63.0	582	1	ZP36_HUMAN
39	34	63.0	711	1	HGFL_HUMAN
40	34	63.0	716	1	HGFL_MOUSE
41	34	63.0	1396	1	VLTF_BPTS
42	33	61.1	61	1	XYLU_BCOLI
43	33	61.1	108	1	KV1V_HUMAN
44	33	61.1	108	1	Y388_MYCEN
45	33	61.1	245	1	DWA_SQUAC

ALIGNMENTS

RESULT 1	ID	KV3M_HUMAN	STANDARD	PRT	129 AA
AC	P18136				
DT	01-NOV-1990 (Rel. 16, Created)				
DT	01-NOV-1990 (Rel. 16, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	IG kappa chain V-III region HIC precursor.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxId=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=88171307; PubMed=3127527;				
RA	Kappa T.J., Tomhave B., Chen P.P., Carson D.A.				
RT	"Antibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy."				
RT	J. Exp. Med. 167:840-852(1988).				
RU	-1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M				
CC	-1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M				
CC	AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCTIC				
CC	LEUKEMIA.				
DR	PIR, P10021; KAHMT.				
DR	HSSP, P80362; IWL.				
DR	InterPro: IPR003006; IG_MHC.				
DR	InterPro: IPR003596; IG_V.				
DR	Pfam: PF00047; IG_1.				
DR	SMART, SM00406; IG_1.				
KM	Immunoglobulin V region; Signal.				
FT	STGNAL	1	20		
FT	CHAIN	21	129		
FT	DOMAIN	21	43		
FT	DOMAIN	44	55		
FT	DOMAIN	56	70		
FT	DOMAIN	71	77		
FT	DOMAIN	78	109		
FT	DOMAIN	110	118		
FT	DOMAIN	119	129		
FT	DISULFID	43	109		
FT	NON_TER	129	129		
SO	SEQUENCE	129 AA	14070 MW	7395528E2B74D6 CRC64;	

Query Match 100.0%; Score 54; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOYSSPWT 9

DB 110 QOYSSPWT 118

RESULT 2
KV3A_HUMAN STANDARD; PRT; 108 AA.
ID KV3A_HUMAN
AC P01619;

DT 21-JUL-1986 (Rel. 01, Last Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region B6.
 OS Homo sapiens (Human)
 CC Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RX NCBI_TaxID=9606;
 RP SEQUENCE.
 RA Milstein C.;
 RT "The basic sequences of immunoglobulin kappa chains: sequence studies
 of Bence Jones proteins Rad, F4 and B6."
 RL FEBS Lett 2:301-304(1969).
 CC -1- MISCELLANEOUS: THIS IS A BENGE-JONES PROTEIN.
 DR HSSP; P80362; 1WT.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig_V.
 DR SMART; SM00406; IGV; 1.
 DR KAM; SM00406; IGV; 1.
 KM Immunoglobulin V region; Bence-Jones protein.
 FT DISULFID 23
 FT NON TER 89 BY SIMILARITY.
 SQ SEQUENCE 108 AA; 11635 MW; 8BCLAF07A419E3D CRC64;
 QY 1 QYSSSPT 9
 Db 90 QYSSSPT 98
 Query Match 81.5%; Score 44; DB 1; Length 108;
 Best Local Similarity 88.9%; Pred. No. 0.29;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 RESULT 3
 ID KVS3 HUMAN STANDARD; PRT; 130 AA.
 AC P01639; P01640;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-V region MOPC 41 precursor.
 OS Mus musculus (Mouse).
 CC Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RX NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RA Feldman J.G.; Max E.E.; Leder P.;
 RT "A kappa-immunoglobulin gene is formed by site-specific recombination
 without further somatic mutation."
 RL Nature 280:370-375(1979).
 RN [2]
 RP SEQUENCE OF 1-33.
 RX MEDLINE=7221900; PubMed=403522;
 RA Birstein Y.; Schenker I.;
 RT "Amino acid sequence of the NH2-terminal extra piece segments of the
 precursors of mouse immunoglobulin lambda-type and kappa-type light
 chains."
 RL Proc. Natl. Acad. Sci. U.S.A. 74:716-720(1977).
 RN [3]
 RP SEQUENCE OF 23-130.
 RX MEDLINE=67056897; PubMed=4162931;
 RA Gray W.R.; Dreyer W.J.; Hood L.;
 RT "Mechanism of antibody synthesis: size differences between mouse
 kappa chains."
 RL Science 155:465-467(1967).
 CC -1- MISCELLANEOUS: THIS PRECURSOR WAS SYNTHESIZED IN A CELL-FREE
 CC SYSTEM DIRECTED BY mRNA ISOLATED FROM MYELOMA POLYSOMES.
 DR PIR; A01922; KWSM4.

DR HSSP; P01607; IREI.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig_V.
 DR SMART; SM00406; IGV; 1.
 KM Immunoglobulin V region; Signal; Bence-Jones protein.
 FT SIGNAL 1
 FT CHAIN 23
 FT DOMAIN 23 130
 FT DOMAIN 23 45
 FT DOMAIN 46 56
 FT DOMAIN 57 71
 FT DOMAIN 72 78
 FT DOMAIN 111 110
 FT DOMAIN 111 119
 FT DOMAIN 120 129
 FT DISULFID 45 110
 FT VARIANT 1 2
 FT NON TER 130
 SQ SEQUENCE 130 AA; 14311 MW; 5EF0E71DSF1BEC CRC64;
 QY 2 QYSSSPT 9
 Db 112 QYSSSPT 119
 Query Match 79.6%; Score 43; DB 1; Length 130;
 Best Local Similarity 87.5%; Pred. No. 0.53;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 RESULT 4
 ID KVS3 HUMAN STANDARD; PRT; 109 AA.
 AC P01620;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region SIE.
 OS Homo sapiens (Human).
 CC Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RX NCBI_TaxID=9606;
 RP SEQUENCE.
 RA Andrews D.W.; Capra J.D.;
 RT "Amino acid sequence of the variable regions of light chains from two
 idiotypically cross-reactive human Igm anti-gamma-globulins of the Wa
 group."
 RL Biochemistry 20:5816-5822(1981).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
 GLOBULIN ACTIVITY.
 DR PIR; A01892; KAHUSI.
 DR HSSP; P80362; 1WT.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig_V.
 DR SMART; SM00406; IGV; 1.
 KM Immunoglobulin V region.
 FT DISULFID 23 89 BY SIMILARITY.
 FT NON TER 109
 SQ SEQUENCE 109 AA; 11775 MW; 7689C3BCD646FB4 CRC64;
 QY 1 QYSSSPT 9
 Db 90 QYSSSPT 98
 Query Match 75.9%; Score 41; DB 1; Length 109;
 Best Local Similarity 88.9%; Pred. No. 1;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 RESULT 5
 ID KVS3 HUMAN

Db 90 QQYGSSPLT

RESULT 2

099Y45

ID

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RC

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SQ SEQUENCE 373 AA; 43018 MW; 69B6C39E27CFD46E CRC64;

Query Match

Best Local Similarity

Matches

6; Conservative

1; Mismatches

1; Indels

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SQ SEQUENCE 373 AA; 43018 MW; 69B6C39E27CFD46E CRC64;

Query Match

Best Local Similarity

Matches

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SQ SEQUENCE 373 AA; 43018 MW; 69B6C39E27CFD46E CRC64;

Query Match

Best Local Similarity

Matches

6; Conservative

1; Mismatches

1; Indels

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SQ SEQUENCE 373 AA; 43018 MW; 69B6C39E27CFD46E CRC64;

Query Match

Best Local Similarity

Matches

6; Conservative

1; Mismatches

1; Indels

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GenCore version 5.1.4.DS.4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:56:17 ; Search time 7.13684 Seconds
(Without alignments)

168.037 Million cell updates/sec

Title: US-09-644-668a-35

Perfect score: 54

Sequence: 1 QOYGSSEPT 9

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	9	22	AA67495 Human light chain
2	54	100.0	108	22	AA67495 Human anti-Rh(D) a
3	54	100.0	108	22	AA67495 Human HIV-1 monoclonal
4	51	94.4	108	15	AA67495 Anti-HIV gp120 imm
5	51	94.4	108	17	AA67495 VL region of HIV n
6	51	94.4	108	21	AA67495 Anti-gp120 antibody
7	51	94.4	108	21	AA67495 Anti-gp120 antibody
8	51	94.4	235	21	AA67495 The kappa chain of
9	51	94.4	235	21	AA67495 The kappa chain of
10	45	83.3	8	15	AA67495 Light chain CDR3 f

11	45	83.3	8	17	AA67495
12	45	83.3	11	17	AA67495
13	45	83.3	107	22	AA67495
14	45	83.3	109	22	AA67495
15	45	83.3	129	14	AA67495
16	45	83.3	212	23	AA67495
17	45	83.3	214	18	AA67495
18	45	83.3	214	18	AA67495
19	45	83.3	214	20	AA67495
20	45	83.3	214	20	AA67495
21	45	83.3	214	20	AA67495
22	45	83.3	214	20	AA67495
23	45	83.3	214	20	AA67495
24	45	83.3	214	20	AA67495
25	45	83.3	214	20	AA67495
26	45	83.3	214	20	AA67495
27	45	83.3	214	20	AA67495
28	45	83.3	214	20	AA67495
29	45	83.3	214	20	AA67495
30	45	83.3	214	20	AA67495
31	45	83.3	214	20	AA67495
32	45	83.3	214	20	AA67495
33	45	83.3	214	20	AA67495
34	45	83.3	214	20	AA67495
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39	45	83.3	214	20	AA67495
40	45	83.3	214	20	AA67495
41	45	83.3	214	20	AA67495
42	45	83.3	214	20	AA67495
43	45	83.3	214	20	AA67495
44	45	83.3	214	20	AA67495
45	45	83.3	214	20	AA67495

ALIGNMENTS

RESULT 1	AA67495	AA67495 standard; peptide; 9 AA.
AC	AA67495;	
DT	29-MAY-2001 (first entry)	
XX	Human light chain complementarily determining region 3 (CDR3).	
XX	Complementarily determining region; CDR; immune response; antibody;	
XX	Cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;	
XX	autoimmune disease; infectious disease; inflammation; allergy;	
XX	rheumatoid arthritis; myasthenia gravis; lupus erythematosus;	
XX	multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;	
XX	transplant rejection; graft versus host disease.	
OS	Homo sapiens.	
PN	WO200114424-A2.	
PD	01-MAR-2001.	
XX	24-AUG-2000; 2000MO-US23356.	
PF	24-AUG-1999; 99US-0150452.	
PR	(MEDA-) MEDAREX INC.	
PA	Korman AJ, Halk EL, Lonberg N;	
XX	WPI; 2001-202933/20.	
XX		

Light chain CDR3 o
Random light chain
Human HIV-1 monoclonal
Human HIV-1 monoclonal
VK325-JK2. Homo s
Human telomerase toxo
NAUUC-2 light chain
Ulcerative colitis
Human UC PANCA mon
NAUUC-2 antibody 1
UC PANCA MAb NAUUC
Light chain CDR3 f
Light chain CDR3 o
Synthetic peptide
Anti-IL-4 receptor
Anti-IL-4 and IL-1
Low-risk modified
Moderate-risk modi
Protein SEQ ID NO:
H65 protein sequen
Humanised anti-CD5
Light chain of Mif
Prp 37 light chain
Anti-Prp antibody
Anti-prion protein
PXOM2. Mus muscul
Sequence of the le
MAB GAH variable r
CDR #3 of r101-2 1
Randomised VJ3 seq
Consensus humanise
Human V1 consensus

PT Novel human sequence antibody that binds to human cytotoxic T
 PT lymphocyte associated antigen-4, useful for inducing, augmenting or
 PT prolonging immune response to antigen or for suppressing immune
 PT response in patient

Claim 30; Page 99; 127pp; English.

CC AAB67490-99 and AAB67501-06 represents complementarity determining
 CC regions (CDRs) of human antibodies. The antibodies specifically bind to
 CC human cytotoxic T lymphocyte associated antigen-4 (CTLA-4). Such
 CC antibodies are used in methods for inducing, augmenting or prolonging
 CC an immune response to an antigen in a patient, where the antibodies
 CC block binding of human CTLA-4 to human B7 ligands. The antibodies are
 CC also useful for treating autoimmune disease in a subject caused or
 CC exacerbated by increased activity of T cells and for treating prostate
 CC cancer, melanoma or epithelial cancer. A polyvalent or polyclonal
 CC antibody preparation comprising two antibodies of the invention are
 CC useful for suppressing an immune response in a patient. They are used for
 CC treating cancer, infectious diseases and promoting beneficial autoimmune
 CC components. The polyvalent or polyclonal preparations are useful for
 CC treating autoimmune diseases such as rheumatoid arthritis, myasthenia
 CC gravis and lupus erythematosus, multiple sclerosis, insulin-dependent
 CC diabetes mellitus, transplant rejection, and inflammation, graft versus
 CC host disease.

CC Sequence 9 AA;

Query Match 100.0%; Score 54; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QOYSSSPT 9
 Db 1 QOYSSSPT 9

RESULT 2
 AAG3666
 ID AAG3666 standard; Protein; 108 AA.

AC AAG3666;

DT 14-SEP-2001 (first entry)

DE Human anti-Rh(D) antibody clone SH52 protein sequence.

KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 KW red blood cell; Rh phenotype; diagnosis; therapeutic.

OS Homo sapiens.

PN US6255455-B1.

PD 03-JUL-2001.

PF 29-JAN-1999; 99US-0240274.

PR 11-OCT-1996; 96US-0028550.

PR 10-APR-1998; 98US-0081380.

PR 27-JUN-1997; 97US-0884045.

PA (UYPB-) UNIV PENNSYLVANIA.

PI Siegel DL;

PT WPI, 2001-388931/41.
 PT N-PSDB; AAB68723.
 PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine.

PS Claim 1; Column 70; 162pp; English.

CC The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (I) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG33558 to AAG33669. (I) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAG33558 to AAG33669 represent the nucleotide sequence which encode
 CC chain CDR3 amino acid sequences which are given in the exemplification
 CC of the present invention.

CC Sequence 108 AA;

Query Match 100.0%; Score 54; DB 22; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.079;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QOYSSSPT 9
 Db 89 QOYSSSPT 97

RESULT 3
 AAB62770
 ID AAB62770 standard; Protein; 108 AA.

AC AAB62770;

DT 03-APR-2001 (first entry)

DE Human HIV-1 monoclonal antibody SEQ ID NO: 69.

KW Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
 KW envelope glycoprotein; gp120; diagnosis.

OS Homo sapiens.

PN WO200100678-A1.

PD 04-JAN-2001.

PF 23-JUN-2000; 2000MO-US17327.

PR 30-JUN-1999; 99US-0141701.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Watkins BA, Reitz MS;

DR WPI, 2001-112438/12.

DR N-PSDB; AAF29071.

PT Novel human monoclonal antibody immunoreactive with human
 PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
 PT in biological sample and providing passive immunotherapy to HIV-1
 PT infected mammal

PS Claim 1; Page 66; 81pp; English.

CC The present invention provides the protein and coding sequences for the
 CC variable regions of human monoclonal antibodies which are immunoreactive
 CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
 CC These can be used in diagnosis and therapy of HIV-1 infection.

CC Sequence 108 AA;

Query Match 100.0%; Score 54; DB 22; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.079;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QOYSSPMT 9
 |||||
 Db 89 QOYSSPMT 97

RESULT 4

ID AAR54307 standard; protein; 108 AA.

AC AAR54307;

DT 10-NOV-1994 (first entry)

DE Anti-HIV gp120 immunoglobulin light chain variable region b24.

KM Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
 KW neutralisation; monoclonal antibody; kappa light chain;
 XX variable region; framework; complementarity determining region.
 OS Homo sapiens.

FT key Location/Qualifiers

FT Region 1..21

FT /label= FR1

FT Region 22..33

FT /label= CDR1

FT Region 34..48

FT /label= FR2

FT Region 49..55

FT /label= CDR2

FT Region 56..87

FT /label= FR3

FT Region 88..96

FT /label= CDR3

FT Region 97..108

FT /label= FR4

PN MO9407922-A.

PD 14-APR-1994.

PF 30-SEP-1993; 93WO-US09328.

PR 30-SEP-1992; 92US-0954148.

XX (SCRI) SCRIPPS RES INST.

XX Barbas CF, Burton DR, Lerner RA;

XX .PI; 1994-135516/16.

PT New human monoclonal antibodies neutralising HIV - react with

PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo

PT or in vitro diagnosis and for passive immunotherapy

PS Example; Page 177-178; 248pp; English.

XX Lymphocyte mRNA was converted to cDNA and subjected to PCR

CC amplification using primers specific for heavy and light chain

CC variable regions. The amplification products were inserted into a

CC dicistronic vector to produce a library of fragments. E.coli XL1

CC Blue cells were transformed with the library. Filamentous phage were

CC produced which expressed the Mab regions on their surface. Panning

CC with gp120 and gp41 resulted in the recovery of immunoreactive

CC clones. The light chain VK region sequence AAR54307 is from a gp120-

CC specific clone.

SO Sequence 108 AA;

Query Match 94.4%; Score 51; DB 15; Length 108;

Best Local Similarity 88.9%; Pred. No. 0.26;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 QOYSSPMT 9
 |||||
 Db 88 QOYSSPMT 96

RESULT 5

ID AAM01265 standard; Protein; 108 AA.

AC AAM01265;

DT 28-JAN-1997 (first entry)

DE VL region of HIV neutralising Mab, clone b24.

KM Heavy chain; light chain; variable region; VH; monoclonal antibody;
 KW Mab; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
 XX virus infectivity assay; precursor gp160; immunocompetence; human;
 OS anti-HIV antibody; detection; HIV infection.

FT key Location/Qualifiers

FT Region 1..21

FT /label= FR1

FT Region 22..33

FT /label= CDR1

FT Region 34..48

FT /label= FR2

FT Region 49..55

FT /label= CDR2

FT Region 56..87

FT /label= FR3

FT Region 88..96

FT /label= CDR3

FT Region 97..108

FT /label= FR4

PN MO9602273-A1.

PD 01-FEB-1996.

PF 11-JUL-1995; 95WO-US08743.

PR 18-JUL-1994; 94US-0276852.

XX (SCRI) SCRIPPS RES INST.

XX Barbas CF, Burton DR, Lerner RA;

XX .PI; 1996-179601/18.

PT Monoclonal antibody binding to VL/V2 loop of HIV gp120 - used in

PT passive immunotherapy and detection of HIV infection.

PS Example; Fig 11; 366pp; English.

XX The sequences given in AAM01261-92 represent the light chain variable

CC regions (VL) of a series of monoclonal antibodies (Mab's) which are

CC immunoreactive with HIV glycoprotein gp120 and are capable of

CC neutralising HIV. This sequence represents the sequence of the JKL

CC gene clone, b24. A Mab containing this VL sequence has the capacity

CC to reduce HIV infectivity titre in an in vivo virus infectivity assay

CC by 50 % at a concentration of less than 700 ng of antibody/mL, and

CC binds mature gp120 preferentially over the precursor gp160. The Mab

CC may be used for determining immunocompetence of a human anti-HIV

CC antibody and in the detection of HIV infection.

SO Sequence 108 AA;

Query Match 94.4%; Score 51; DB 17; Length 108;

Best Local Similarity 88.9%; Pred. No. 0.26;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 OQYSSPWT 9
 |||||
 DB 88 OQYGTSPWT 96

RESULT 6
 AAY95117
 ID AAY95117 standard; Protein; 108 AA.

XX AAY95117;

DT 30-JUN-2000 (first entry)

DE Anti-gp120 antibody light chain variable region from clone b24.

XX Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
 KW reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
 KW glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.

OS cmo sapiens.

XX AUY948756-A.

PD 17-FEB-2000.

PF 16-SEP-1999; 99AU-0048756.

PR 16-SEP-1999; 99AU-0048756.

XX (SCRI) SCRIPPS RES INST.

PI Burton DR, Barbas CF, Lerner RA;

WPI; 2000-293393/26.

PT Novel human monoclonal antibodies which immunoreact with and neutralise
 PT human immunodeficiency virus useful for treating HIV infections

XX Example 9; Figure 11; 366pp; English.

XX The present sequence represents a fragment of an anti-human
 CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to
 CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
 CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
 CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an
 CC in vitro virus infectivity assay by 50% at a concentration of less than
 CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and
 CC immunotherapy of HIV induced disease. They are useful as neutralising
 CC field isolates and provide useful information regarding the
 CC immunocompetence of an immune response in HIV infected patients. The
 CC monoclonal antibodies are useful for producing anti-idiotypic antibodies
 CC which can be used to screen human monoclonal antibodies to identify
 CC whether the antibody has the same binding specificity as the antibodies
 CC of the invention. The neutralising antibodies define new epitopes on the
 CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of new
 CC immunotherapeutic human monoclonal antibodies. A major advantage of the
 CC monoclonal antibodies derives from the fact that they are encoded by a
 CC human polynucleotide sequence. Thus in vivo use of the monoclonal
 CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly
 CC reduces the problems of significant host immune response to the passively
 CC administered antibodies which is a problem commonly encountered when
 CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
 CC An additional major advantage of the monoclonal antibodies described
 CC derives from the fact that they immunoreact with a unique determinant
 CC present on mature HIV glycoprotein gp120. This class of antibodies is
 CC particularly effective at neutralising field isolates of HIV.

XX Sequence: 108 AA;

Query Match 94.4%; Score 51; DB 21; Length 108;
 Best Local Similarity 88.9%; Pred. No. 0.26;
 Matches 89 Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 OQYSSPWT 9
 |||||
 DB 88 OQYGTSPWT 96

RESULT 7
 AAY98226
 ID AAY98226 standard; Protein; 108 AA.

XX AAY98226;

DT 04-JUN-2000 (first entry)

DE Anti-gp120 antibody light chain variable region from clone b24.

XX Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
 KW human immunodeficiency virus type 1; HIV-1; infectivity titre;
 KW passive immunotherapy; reduce severity; HIV-induced disease;
 KW immunocompetence; active immunisation.

OS Homo sapiens.

XX AUY948754-A.

PD 17-FEB-2000.

PF 16-SEP-1999; 99AU-0048754.

PR 16-SEP-1999; 99AU-0048754.

XX (SCRI) SCRIPPS RES INST.

PI Burton DR, Barbas CF, Lerner RA;

WPI; 2000-246867/22.

PT Human neutralizing monoclonal antibodies to human immunodeficiency
 PT virus (HIV) used for providing passive immunotherapy to HIV are
 PT specific for glycoprotein-120

XX Example 9; Figure 11; 374pp; English.

XX This sequence represents a fragment of the antibodies of the invention.
 CC The invention relates to the production of an anti-HIV (human
 CC immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody
 CC capable of reducing an HIV infectivity titre in an in vitro virus
 CC infectivity assay by 50% at a concentration of less than 70 ng/ml. The
 CC method for the production of the antibody comprises:
 CC (a) providing a first polynucleotide encoding a heavy chain
 CC immunoglobulin amino acid sequence (which does not comprise the sequence
 CC represented by AAY98206) and a second polynucleotide encoding a light
 CC chain immunoglobulin amino acid sequence;
 CC (b) inserting the first and second polynucleotide sequences into a host
 CC cell;
 CC (c) maintaining the host cell in conditions which allow the amino acid
 CC sequences encoded by the polynucleotides to be expressed in the host
 CC cell; and
 CC (d) isolating the antibody comprising the heavy and light chain
 CC immunoglobulin amino acid sequences from the host cell.
 CC The anti-HIV gp-120 monoclonal antibody is used for providing passive
 CC immunotherapy to HIV in a human. They can be administered to high-risk
 CC patients to reduce the likelihood and/or severity of HIV-induced disease
 CC and to patients who are already HIV-infected. The antibodies are used
 CC for neutralising field isolates which provides information about the
 CC immunocompetence of an immune response in HIV patients, for detecting
 CC HIV in a biological fluid or tissue sample e.g. by radioimmunoassay, for
 CC producing anti-idiotypic antibodies which can be used for active
 CC immunisation and to screen human monoclonal antibodies to identify those
 CC with the same binding specificity and to monitor the course of HIV
 CC disease therapy by measuring the changes in concentration of HIV present
 CC in the body or in body fluids by immunoassay. The anti-HIV gp-120
 CC monoclonal antibodies are encoded by a human polynucleotide sequence and

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OM protein - protein search, using SW model

Run on: April 16, 2003, 17:21:54 ; Search time 2.65263 Seconds

(without alignments)
256.547 Million cell updates/sec

Title: US-09-644-668a-35

Sequence: 1 QOYGSFPT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 288829 seqs, 7561385 residues

Total number of hits satisfying chosen parameters: 288829

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	45	83.3	212	9	US-10-006-593-118 Sequence 118, App
3	43	79.6	109	10	US-09-843-906-74 Sequence 74, App
4	42	77.8	108	10	US-09-056-160B-12 Sequence 12, App
5	42	77.8	109	10	US-09-811-123-6 Sequence 6, App
6	42	77.8	249	9	US-10-237-867-18 Sequence 18, App
7	42	77.8	249	9	US-10-237-867-18 Sequence 18, App
8	42	77.8	249	9	US-10-237-867-18 Sequence 18, App
9	42	77.8	249	9	US-10-237-867-18 Sequence 18, App
10	42	77.8	249	9	US-10-237-867-18 Sequence 18, App
11	41	75.9	150	9	US-09-884-186-18 Sequence 18, App
12	41	75.9	287	9	US-09-782-397-5 Sequence 5, App
13	41	75.9	304	9	US-09-782-397-17 Sequence 17, App
14	40	74.1	9	10	US-09-056-160B-125 Sequence 125, App
15	40	74.1	9	10	US-09-828-708-52 Sequence 52, App
16	40	74.1	9	10	US-09-828-708-56 Sequence 56, App
17	40	74.1	105	10	US-09-828-708-3 Sequence 3, App
18	40	74.1	105	10	US-09-828-708-7 Sequence 7, App
19	40	74.1	107	8	US-08-844-215-10 Sequence 10, App

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21	40	74.1	253	9	US-09-880-748-1499 Sequence 1499, App
22	40	74.1	261	9	US-10-231-013-13 Sequence 13, App
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27	39	72.2	108	9	US-10-153-159-4 Sequence 4, App
28	39	72.2	108	9	US-10-153-159-16 Sequence 16, App
29	39	72.2	108	9	US-10-153-176-2 Sequence 2, App
30	39	72.2	108	9	US-10-153-176-4 Sequence 4, App
31	39	72.2	108	9	US-10-153-176-16 Sequence 16, App
32	39	72.2	108	10	US-09-056-160B-8 Sequence 8, App
33	39	72.2	108	10	US-09-056-160B-10 Sequence 10, App
34	39	72.2	108	10	US-09-056-160B-126 Sequence 126, App
35	39	72.2	108	10	US-09-056-160B-103 Sequence 103, App
36	39	72.2	110	10	US-09-056-160B-105 Sequence 105, App
37	39	72.2	110	10	US-09-056-160B-107 Sequence 107, App
38	39	72.2	110	10	US-09-056-160B-109 Sequence 109, App
39	39	72.2	110	10	US-09-056-160B-111 Sequence 111, App
40	39	72.2	110	10	US-09-056-160B-113 Sequence 113, App
41	39	72.2	110	10	US-09-056-160B-115 Sequence 115, App
42	39	72.2	110	10	US-09-056-160B-117 Sequence 117, App
43	39	72.2	154	9	US-09-925-299-1226 Sequence 1226, App
44	39	72.2	154	10	US-09-925-299-1226 Sequence 1226, App
45	39	72.2	237	10	US-09-056-160B-100 Sequence 100, App

ALIGNMENTS

RESULT 1
US-09-848-798-178
Sequence 178, Application US/09848798
Publication No. US2003040605A1
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/848,798
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 178
LENGTH: 108
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH52
US-09-848-798-178

Query Match 100.0%; Score 54; DB 9; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOYGSFPT 9
DB 89 QOYGSFPT 97

RESULT 2
US-10-006-593-118
Sequence 118, Application US/10006593
Publication No. US20030049683A1
GENERAL INFORMATION:
APPLICANT: Bowdler, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Renshaw, Mark

TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
FILE REFERENCE: 1087-2
CURRENT APPLICATION NUMBER: US/10/006,593
CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: US 60/288,889
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patent version 3.1
SEQ ID NO: 118
LENGTH: 212
TYPE: PRT
ORGANISM: human
US-10-006-593-118

Query Match 83.3%; Score 45; DB 9; Length 212;
Best Local Similarity 87.5%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOYSSPWT 8
DB 88 QOYSSPWT 95

RESULT 3

US-09-943-906-74
Sequence 74, Application US/09943906
Patent No. US20020150571A1
GENERAL INFORMATION:

APPLICANT: Prusiner, Stanley B.

Williamson, R. Anthony

Burton, Dennis R.

TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP

NUMBER OF SEQUENCES: 86

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 2200 Sand Hill Road

CITY: Menlo Park

STATE: CA

COUNTRY: U.S.A.

ZIP: 94025

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/943,906

FILING DATE: 30-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/550,374

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Bozicevic, Karl

REGISTRATION NUMBER: 28,807

REFERENCE/DOCKET NUMBER: 06510/059001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-854-5277

TELEFAX: 415-854-0875

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 74:

SEQUENCE CHARACTERISTICS:

LENGTH: 109 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 74:

US-09-943-906-74

Query Match 79.6%; Score 43; DB 10; Length 109;
Best Local Similarity 87.5%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QOYSSPWT 9
DB 90 QOYSSPWT 97

RESULT 4

US-09-056-160B-12
Sequence 12, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:

APPLICANT: Baca, Manuel

APPLICANT: Wells, James A.

APPLICANT: Presta, Leonard G.

APPLICANT: Lowman, Henry B.

APPLICANT: Chen, Yvonne M.

TITLE OF INVENTION: ANTI-VEGF ANTIBODIES

NUMBER OF SEQUENCES: 131

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/056,160B

FILING DATE: 06-Apr-1998

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/054,856

FILING DATE: 06-Aug-1997

ATTORNEY/AGENT INFORMATION:

NAME: Haasek, Janet E.

REGISTRATION NUMBER: 28,616

REFERENCE/DOCKET NUMBER: P1093R2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/952-9881

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 108 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-09-056-160B-12

Query Match 77.8%; Score 42; DB 10; Length 108;

Best Local Similarity 77.8%; Pred. No. 2.6;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOYSSPWT 9
DB 89 QOYSSPWT 97

RESULT 5

US-09-811-123-6

Sequence 6, Application US/0981123

Patent No. US20020001587A1

GENERAL INFORMATION:

APPLICANT: Sharon Erickson

APPLICANT: Ralph Schwall

APPLICANT: Mark Sliwkowski

TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-erbB

CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-276-852-86

Query Match 94.4%; Score 51; DB 1; Length 108;
Best Local Similarity 88.9%; Pred. No. 0.037;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOYGSSEPT 9
DB 88 QOYGSSEPT 96

RESULT 3
US-08-899-575-86
Sequence 86, Application US/08899575
GENERAL INFORMATION:
PATENT NO. 5770440
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSER: Patent Counsel
STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
CITY: Mail Drop TPC8
STATE: La Jolla
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-86

Query Match 94.4%; Score 51; DB 1; Length 108;
Best Local Similarity 88.9%; Pred. No. 0.037;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOYGSSEPT 9
DB 88 QOYGSSEPT 96

RESULT 4
US-08-899-575-86
Sequence 86, Application US/08899575
GENERAL INFORMATION:
PATENT NO. 5804440
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSER: Patent Counsel
STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
CITY: Mail Drop TPC8
STATE: La Jolla
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:

1	43	74.1	365	2	156197	Fe gamma (19g) rece
2	42	72.4	970	2	P64230	spore germination
3	41	70.7	286	2	T03434	probable transport
4	41	70.7	286	2	AE3245	hypothetical prote
5	40	69.0	214	2	AG3525	NADH2 dehydrogenas
6	39	67.2	365	2	JCS604	hydrolase family p
7	39	67.2	365	2	138720	ABC-transporting p
8	39	67.2	401	2	S75788	hCtn - human
9	39	67.2	401	2	S75788	histidine-CRNA 11g
10	39	67.2	401	2	H75554	NiS-related prote
11	39	67.2	401	2	T09906	hypothetical prote
12	39	67.2	887	2	S73768	MG277 homolog Fil
13	38	65.5	143	2	S17939	xpgC protein - Xan
14	38	65.5	344	2	S62765	NADH2 dehydrogenas
15	37	63.8	69	2	B45252	P1V variable regi
16	37	63.8	170	2	S33553	beta-fructofuranos
17	37	63.8	213	2	S68213	Ig heavy chain (Mac
18	37	63.8	377	2	AH3328	NAD(PAD)-utilizing
19	37	63.8	393	2	EB7432	conserved hypotet
20	37	63.8	394	2	AF2650	conserved hypotet
21	37	63.8	398	2	AE2366	conserved hypotet
22	37	63.8	398	2	GH0482	conserved hypotet
23	37	63.8	400	2	G65146	hypothetical 43.8
24	37	63.8	400	2	D91174	hypothetical prote
25	37	63.8	400	2	D86020	hypothetical prote
26	37	63.8	400	2	AD0988	probable exported
27	37	63.8	401	2	G64161	hypothetical prote
28	37	63.8	420	2	E97432	hypothetical prote
29	37	63.8	430	2	B26421	shufflon A - Esch

30	37	63.8	473	2	T06167	beta-fructofuranosyl
31	37	63.8	788	2	I51530	integrin beta-3 su
32	37	63.8	968	2	E90481	alpha-mannosidase
33	36	62.1	106	2	E72239	hypothetical prote
34	36	62.1	125	2	S24703	ig heavy chain v6
35	36	62.1	254	2	F70961	hypothetical prote
36	36	62.1	311	2	A81880	hypothetical prote
37	36	62.1	314	2	H88991	protein K08D9.1 (1
38	36	62.1	346	2	F82349	ADP-nepcase-LPS ha
39	36	62.1	372	2	S60207	fomf protein - Strc
40	36	62.1	408	2	AC2198	hypothetical prote
41	36	62.1	540	2	AG2161	GMP synthase (glut
42	36	62.1	542	2	S76358	GMP synthase (glut
43	36	62.1	566	1	YDBPA7	DNA primase - phag
44	36	62.1	566	1	S07508	DNA primase - phag
45	36	62.1	694	2	S56060	long-chain-fatty-a

ALIGNMENTS

RESULT 1

I56197

C;Species: Mus musculus (house mouse)

C/Accession: I56197; I49661

J. Immunol. 151, 6076-6088, 1993

A;Reference number: I56197; MUID:94065162; PMID:7504013

A/Status: preliminary; translated from GB/EMBL/DBJ

A;Residue: 1-365 <RES>

R;Kandil, E.; Noguchi, M.; Ishibashi, T.; Kasahara, M.

A; Title: Structural and phylogenetic analysis of the MHC class I-like Fc receptor gene

A:Accession: I496661

A;Molecule type: mRNA

A; Cross-references: GB:D37874; NID:g1009353; PIDN:BAA07111.1; PID:g1009354

A;Gene: FcRn

C/keywords: immunoglobulin receptor

Query Match 74.18; Score 43; DB 2; Length 365

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGM LGPE DY 9

Db 48 TGLGPQQY 56

RESULT 2

F64230

C/Species: Mycoplasma genitalium

C:\Accession: F64230

M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.

Science 270, 397-403, 1995

A;Reference number: A64200; MUID:96026346; PMID:7569993

A; Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA
 A/Residues: 1-970 <TIGR>
 A/Cross-references: GB:U39707; GB:U43967; NID:G3844865; PIDN:AACT1499.1; PID:G1045972, T
 A/Experimental source: strain G-37
 C/Genetics:
 A/Genetic code: SGC3
 A/Start codon: GTG

Query Match 72.4%; Score 42; DB 2; Length 970;
 Best Local Similarity 75.0%; Pred. No. 23;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 GWLGPFDY 9
 DB 932 GWLSPFNY 939

RESULT 3
 T03434
 A/Molecule type: accb - Agrobacterium tumefaciens plasmid pTIC58
 C/Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999
 C/Accession: T03434
 R/Piper, K.R.; Beck von Bodman, S.; Cook, D.M.; Hwang, I.; Kim, H.; Farrand, S.K.
 submitted to the EMBL Data Library, May 1998
 A/Reference number: Z14943
 A/Accession: T03434
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-286 <PIP>
 A/Cross-references: EMBL:AF010180; NID:G3153171; PIDN:AACT17201.1; PID:G3153181
 C/Genetics:
 A/Genetic code: accb
 A/Genome: plasmid pTIC58
 C/Superfamily: oligopeptide permease protein oppb

Query Match 70.7%; Score 41; DB 2; Length 286;
 Best Local Similarity 85.7%; Pred. No. 9.4;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 WLGPFY 9
 DB 43 WLAFFDY 49

RESULT 4
 AB3245
 A/Molecule type: accb [imported] - Agrobacterium tumefaciens (strain C58, Dupont) pl
 C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
 C/Accession: AB3245
 R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
 et al.; G. J. Gill, W.; Grant, C.; Gentner, D.; Kutyav, T.; Levy, R.; Li, M.; Mclell
 Science 294, 2317-2323, 2001
 A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, B.W.
 A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A/Reference number: AB3245; PMID:11743193
 A/Accession: AB3245
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-286 <KUR>
 A/Cross-references: GB:AE008690; PIDN:AAU46379.1; PID:G17744171; GSPDB:GN00189
 A/Experimental source: strain C58 (Dupont)
 C/Genetics:
 A/Genetic code: accb
 A/Genome: plasmid
 C/Superfamily: oligopeptide permease protein oppb

Query Match 70.7%; Score 41; DB 2; Length 286;
 Best Local Similarity 85.7%; Pred. No. 9.4;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WLGPFY 9
 DB 43 WLAFFDY 49

RESULT 5
 T11938
 A/Molecule type: accb (ubiquinone) (EC 1.6.5.3) chain 1 - Prototheca wickerhamii mitoc
 C/Species: mitochondrion Prototheca wickerhamii
 C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002
 C/Accession: T11938
 R/Moff, G.; Plante, I.; Lang, B.F.; Kueck, U.; Burger, G.
 J. Mol. Biol. 237, 75-86, 1994
 A/Title: Complete sequence of the mitochondrial DNA of the chlorophyte alga Protothec
 A/Reference number: Z17373; MUID:94180393; PMID:8133522
 A/Accession: T11938
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-328 <WOL>
 A/Cross-references: EMBL:U02970; NID:G467843; PID:G467870; PIDN:AAU12657.1
 A/Experimental source: strain 263-11
 C/Genetics:
 A/Genome: mitochondrion
 A/Note: nad1
 C/Superfamily: NADH dehydrogenase (ubiquinone) chain 1
 C/Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation

Query Match 70.7%; Score 41; DB 2; Length 328;
 Best Local Similarity 75.0%; Pred. No. 11;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 WLGPFY 9
 DB 253 GWLPPDF 260

RESULT 6
 AG3525
 A/Molecule type: accb [imported] - Brucella melitensis (strain 16M)
 C/Species: Brucella melitensis
 C/Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
 C/Accession: AG3525
 R/DelVecchio, V.G.; Kapral, V.; Redkar, R.D.; Patra, G.; Mui, C.; Los, T.; Ivanov
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A/Title: The genome sequence of the facultative intracellular pathogen Brucella melit
 A/Reference number: AG3525; PMID:11756688
 A/Accession: AG3525
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-214 <KUR>
 A/Cross-references: GB:AE008918; PIDN:AAU53370.1; PID:G17984261; GSPDB:GN00191
 A/Experimental source: strain 16M
 C/Genetics:
 A/Genetic code: BME110129
 A/Genome: BME110129
 A/Map position: 11

Query Match 69.0%; Score 40; DB 2; Length 214;
 Best Local Similarity 85.7%; Pred. No. 10;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 WLGPFY 8
 DB 36 GWLPPDF 42

RESULT 7
 J05604
 A/Molecule type: accb [imported] - human
 C/Species: Homo sapiens (man)
 C/Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 02-Feb-2001
 C/Accession: J05604

GenCore version 5.1.4.P5 4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:57:42 ; Search time 1.76842 Seconds
(Without alignments)
211.085 Million cell updates/sec

Title: US-09-644-668a-37
Perfect score: 58
Sequence: 1 TGMGPFDPY 9

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	43	74.1	365 1	FCGN_MOUSE
2	42	72.4	970 1	Y277_MYCGE
3	41	70.7	499 1	OPB1_PATYR
4	39.5	68.1	606 1	ABD4_HUMAN
5	39.5	68.1	606 1	ABD4_MOUSE
6	39	67.2	365 1	FCGN_HUMAN
7	39	67.2	401 1	HIS2_SUNY2
8	38	65.5	143 1	Y277_MYCPN
9	38	65.5	143 1	GSPG_XANCP
10	38	65.5	144 1	NUIM_CVACA
11	37	63.8	118 1	GHR1_PIG
12	37	63.8	400 1	YHIN_ECOLI
13	37	63.8	430 1	YHIN_HAENI
14	37	63.8	430 1	SHU2_ECOLI
15	36	62.1	304 1	HEW2_THEVO
16	36	62.1	308 1	HEW2_THBAC
17	36	62.1	343 1	HMAA_TRICA
18	36	62.1	542 1	GUA4_SUNY3
19	36	62.1	566 1	PRIM_BPT3
20	36	62.1	566 1	PRIM_BPT7
21	36	62.1	694 1	LCF4_YEAST
22	35.5	61.2	403 1	Y411_ARATH
23	35	60.3	108 1	MAVI_COCP
24	35	60.3	269 1	EXOK_RHIME
25	35	60.3	318 1	MPD1_YEAST
26	35	60.3	322 1	NUOH_BUCAL
27	35	60.3	366 1	FCGN_RAT
28	35	60.3	431 1	ORDL_HAENI
29	35	60.3	433 1	GAG_HIV2
30	35	60.3	478 1	RECQ_SUNY3
31	35	60.3	551 1	COX1_SUNY3
32	34	58.6	174 1	IHBB_RAT
33	34	58.6	212 1	YOL5_CAEEL

34	34	58.6	256 1	CB2_CHIMO	P22686 chlamydomon
35	34	58.6	259 1	RPRD_YEREN	Q56802 yersinia en
36	34	58.6	260 1	YFAK_ECOLI	P77732 escherichia
37	34	58.6	286 1	CYSW_SUNY7	P27370 synchococc
38	34	58.6	307 1	SYPH_BOVIN	P20488 bos taurus
39	34	58.6	307 1	SYPH_RAT	P07825 rattus norv
40	34	58.6	308 1	SYPH_MOUSE	O62377 mus musculu
41	34	58.6	313 1	SYPH_HUMAN	P08247 homo sapien
42	34	58.6	375 1	MCK1_YEAST	P21965 saccharomyc
43	34	58.6	391 1	NUCC_MESVI	Q9mu10 mesostigma
44	34	58.6	392 1	NUCC_MARPO	P12131 marchantia
45	34	58.6	393 1	NUCC_ARATH	P56753 arabidopsis

ALIGNMENTS

RESULT 1
FCGN_MOUSE
ID FCGN_MOUSE STANDARD; PRT; 365 AA.
AC 061559;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE IGG receptor FCGN large subunit p51 precursor (FCRN) (Neonatal FC receptor) (IGG FC fragment receptor transporter, alpha chain).
GN FCGRT OR FCGN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Small intestine;
RX MEDLINE=95270984; PubMed=7538537;
RA Kandil E., Noguera M., Ishibashi T., Kasahara M.;
RT "Structural and phylogenetic analysis of the MHC class I-like Fc receptor gene.";
RL J. Immunol. 154:5907-5918 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Small intestine;
RX MEDLINE=94065162; PubMed=7504013;
RA Ahoune U.J., Hagerman C.L., Mital P., Gilbert D.J.,
RA Copeland N.G., Jenkins N.A., Simister N.B.;
RT "Mouse MHC class I-like Fc receptor encoded outside the MHC.";
RL J. Immunol. 151:6076-6088 (1993).
CC - FUNCTION: BINDS TO THE FC REGION OF MONOMERIC IMMUNOGLOBULINS
CC GAMMA. MEDIATES THE SELECTIVE UPTAKE OF IGG FROM MILK AND HELPS
CC NEWBORN ANIMALS TO ACQUIRE PASSIVE IMMUNITY. IGG IN THE MILK IS
CC BOUND AT THE APICAL SURFACE OF THE INTESTINAL EPITHELIUM. THE
CC INTESTINAL FCGN-IGG COMPLEXES ARE TRANSCYTOSED ACROSS THE
CC INTESTINAL EPITHELIUM AND IGG IS RELEASED FROM FCGN INTO BLOOD OR
CC TISSUE FLUIDS.
CC - SUBUNIT: FCGN COMPLEX CONSIST OF TWO SUBUNITS: P51, AND P14 WHICH
CC IS EQUIVALENT TO BETA-2-MICROGLOBULIN. IT FORMS AN MCH CLASS I-
CC LIKE HETERODIMER.
CC - SUBCELLULAR LOCATION: Type I membrane protein.
CC - TISSUE SPECIFICITY: INTESTINAL EPITHELIUM OF SUCKLING RODENTS.
CC EXPRESSED IN NEONATAL INTESTINE AND FETAL YOLK SAC.
CC - SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL, D37874; BAA07111.1; -
CC EMBL, D37873; BAA07110.1; -
CC EMBL, D37872; BAA07110.1; JOINED.

DR EMBL; L17022; AAA16904.1; -
 DR HSPB; P13599; 3FRU.
 DR MGD; MGI:103017; Fcgrt.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig_C.
 DR InterPro; IPR01039; MHC_I.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00129; MHC_I; 1.
 DR Prodom; PD000050; MHC_I; 1.
 DR SMART; SM00407; IgC1; 1.
 DR PROSITE; PS00290; Ig_MHC; 1.
 DR IgG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
 KW Immunoglobulin domain; Polymorphism.
 FT SIGNAL 1 21
 FT CHAIN 22 365
 FT DOMAIN 22 110
 FT DOMAIN 111 200
 FT DOMAIN 201 290
 FT DOMAIN 291 297
 FT TRANSMEM 298 321
 FT MAIN 322 365
 FT DISULFID 119 182
 FT DISULFID 221 275
 FT CARBOHYD 108 108
 FT CARBOHYD 125 125
 FT CARBOHYD 149 149
 FT CARBOHYD 246 246
 FT VARIANT 73 73
 FT VARIANT 111 111
 SQ SEQUENCE 365 AA; 40092 MW; 0A2290A54507E0C4 CRC64;

Query Match Best Local Similarity 74.1%; Score 43; DB 1; Length 365;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 DB 48 TWLGPQY 56

RESULT 2
 ID Y277_MYCGE STANDARD; PRT; 970 AA.
 AC Q49409; Q49253;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DB Hypothetical protein MG277.
 GN MG277.
 OS Mycoplasma genitalium.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID:2097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 33530 / G-37;
 RA MEDLINE=96026346; PubMed=7569993;
 RA Frazer C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
 RA Fleischman R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
 RA Nguyen D.T., Weidman J.F., Small K.V., Sandusky M., Fuhmann J.L.,
 RA Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Luster T.S.,
 RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
 RT "The minimal gene complement of Mycoplasma genitalium.";
 RL Science 270:397-403(1995).
 RN [2]
 RP SEQUENCE OF 624-678 FROM N.A.
 RC STRAIN=ATCC 33530 / G-37;
 RA MEDLINE=94075230; PubMed=8253680;
 RA Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III,
 RT "A survey of the Mycoplasma genitalium genome by using random
 sequencing.";
 RL J. Bacteriol. 175:7918-7930(1993).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC CC
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 CC or send an email to license@sib-sib.ch).
 CC
 DR EMBL; U39707; AAC71499.1; -
 DR EMBL; U02116; AAD12390.1; -
 DR TIGR; MG277; -
 KW Hypothetical protein; Transmembrane; Complete proteome.
 FT SIGNAL 1 31
 FT TRANSMEM 11 515
 FT TRANSMEM 515 535
 FT TRANSMEM 537 557
 FT TRANSMEM 558 578
 FT TRANSMEM 614 634
 FT TRANSMEM 645 665
 FT TRANSMEM 726 746
 FT TRANSMEM 762 782
 FT TRANSMEM 789 809
 FT TRANSMEM 816 836
 FT TRANSMEM 877 897
 FT TRANSMEM 903 923
 FT DOMAIN 50 53
 FT DOMAIN 370 382
 FT CONFLICT 673 678
 SQ SEQUENCE 970 AA; 108163 MW; F106CDFCC9BD44FF CRC64;

Query Match Best Local Similarity 72.4%; Score 42; DB 1; Length 970;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 DB 932 GWLSPFN 939

RESULT 3
 ID OP81_PATYE STANDARD; PRT; 499 AA.
 AC O15973;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Rhodopsin, Gq-coupled (Gq-rhodopsin).
 GN SCOP1.
 OS Pectenopterus yessoensis (Ezo giant scallop) (Yesso scallop).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoida;
 OC Pectinoida; Pectinidae; Mizuhopecten.
 OX NCBI_TaxID=6573;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RA MEDLINE=97435252; PubMed=9287291;
 RA Kojima D., Terakita A., Ishikawa T., Tsukahara Y., Maeda A.,
 RA Shichida Y.;
 RT "A novel Gq-mediated phototransduction cascade in scallop visual
 cells.";
 RL J. Biol. Chem. 272:22979-22989(1997).
 CC -1- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT
 CC MEDIANE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY
 CC LINKED TO CIS-RETINAL.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: RETINA. EXPRESSED IN THE DEPOLARIZING CELL
 CC LAYER OF THE PHOTORECEPTOR CELLS DISTANT FROM THE LENS.
 CC -1- PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES MAY
 CC BE PHOSPHORYLATED (BY SIMILARITY)
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC OPSIN SUBFAMILY.
 CC
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OM protein - protein search, using sw model

Run on: April 16, 2003, 17:13:59 / Search time 9.22105 Seconds
(without alignments)
201.108 Million cell updates/sec

Title: US-09-644-668a-37

Perfect score: 58

Sequence: 1 TGMGPFDFY 9

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_21.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeal:

Result No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	74.1	177	11 Q9R2A5	Q9R2A5 mus musculus
2	43	74.1	177	11 Q9R2A5	Q9R2A5 mus musculus
3	41	70.7	286	2 Q30544	Q30544 agrobacteri
4	41	70.7	286	2 Q30544	Q30544 agrobacteri
5	41	70.7	286	2 Q30544	Q30544 agrobacteri
6	41	70.7	286	2 Q30544	Q30544 agrobacteri
7	41	70.7	286	2 Q30544	Q30544 agrobacteri
8	41	70.7	286	2 Q30544	Q30544 agrobacteri
9	41	70.7	286	2 Q30544	Q30544 agrobacteri
10	39.5	68.1	606	4 Q8YD6	Q8YD6 mus musculus
11	39	67.2	81	4 Q75996	Q75996 mus musculus
12	39	67.2	212	4 Q9TW3	Q9TW3 mus musculus
13	39	67.2	250	13 Q9W67	Q9W67 mus musculus
14	39	67.2	251	10 Q94172	Q94172 cyta sativ
15	39	67.2	269	10 Q94E27	Q94E27 cyta sativ
16	39	67.2	273	9 Q9WCP8	Q9WCP8 bacterioph

17	39	67.2	335	2 Q9KGM2	Q9KGM2 pseudomonas
18	39	67.2	362	4 Q9HBV7	Q9HBV7 mus musculus
19	39	67.2	365	4 Q9R219	Q9R219 mus musculus
20	39	67.2	365	4 Q9R219	Q9R219 mus musculus
21	39	67.2	401	16 Q9RY03	Q9RY03 delinococcus
22	39	67.2	487	10 Q9J290	Q9J290 arabidopsis
23	39	67.2	577	4 Q9TKM5	Q9TKM5 mus musculus
24	39	67.2	591	4 Q9TKM5	Q9TKM5 mus musculus
25	39	67.2	599	4 Q8WU48	Q8WU48 mus musculus
26	39	67.2	646	10 Q9STV1	Q9STV1 mus musculus
27	39	67.2	660	4 Q9EGD3	Q9EGD3 mus musculus
28	39	67.2	664	11 Q9JMG0	Q9JMG0 mus musculus
29	39	67.2	700	4 Q9UQRO	Q9UQRO mus musculus
30	39	67.2	719	16 Q8XWU4	Q8XWU4 mus musculus
31	39	67.2	722	11 Q99MW4	Q99MW4 mus musculus
32	39	67.2	877	5 Q24191	Q24191 dirosophila
33	39	67.2	877	5 Q9VHA0	Q9VHA0 dirosophila
34	39	67.2	168	16 Q8XVW3	Q8XVW3 ralsontia s
35	39	67.2	170	10 Q43076	Q43076 avena sativ
36	39	67.2	198	12 Q9QCC7	Q9QCC7 hepatitis c
37	39	67.2	365	2 Q30835	Q30835 rhododactyl
38	39	67.2	377	16 Q8Y131	Q8Y131 bruceella me
39	39	67.2	393	16 Q9A886	Q9A886 caulobacter
40	39	67.2	394	16 Q92RX0	Q92RX0 rhizobium m
41	39	67.2	398	16 Q9KVQ9	Q9KVQ9 vibrio chol
42	39	67.2	398	16 Q8ZUD8	Q8ZUD8 salmonella
43	39	67.2	398	16 Q8ZAS2	Q8ZAS2 yersinia pe
44	39	67.2	400	16 Q8Z267	Q8Z267 salmonella
45	39	67.2	400	16 Q8X5R3	Q8X5R3 escherichia

ALIGNMENTS

RESULT 1	ID	Q9R2A5	PRELIMINARY	PRT	177 AA
AC	Q9R2A5	01-MAY-2000 (TRENBLrel. 13, Created)			
DT	01-MAY-2000 (TRENBLrel. 13, Last sequence update)				
DT	01-JUN-2002 (TRENBLrel. 21, Last annotation update)				
DE	Fc receptor FcRn (Fragment).				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus..				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=P/T;				
RX	MEDLINE=95270984; PubMed=7538537;				
RA	Kandil E., Noguchi M., Ishibashi T., Kasahara M.,				
RT	"Structural and phylogenetic analysis of the MHC class I-like Fc				
RT	receptor gene1."				
RL	J. Immunol. 154:5907-5918(1995).				
DR	EMBL; D37909; BAA07137.1; JOINED.				
DR	EMBL; D37908; BAA07137.1; JOINED.				
DR	HSSP; P13599; 3FRU.				
DR	InterPro; IPR001039; MHC_I.				
DR	Pfam; PF00129; MHC_I.1.				
DR	PRINTS; PR01638; MHCCLASSI.				
DR	ProDom; PD000050; MHC_I.1.				
KW	Receptor.				
FT	NON_TER				
FT	NON_TER				
SC	SEQUENCE 177 AA; 20369 MW; 2290CSBE493933CHD CRC64;				
QY	Query Match	74.1%	Score 43;	DB 11;	Length 177;
DB	Best Local Similarity	77.8%	Pred. No. 6.5;		
	Matches 7;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
	25 TGMGPFDFY 33				

RESULT 2

Q9GUR0 PRELIMINARY; PRT; 177 AA.
 ID Q9GUR0;
 AC Q9GUR0;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DE FC receptor FCrn (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=TW75, C3H, AKR, DBA/2, AND A/J;
 RX MEDLINE=95270984; PubMed=7538537;
 RA Kandil E., Noguchi M., Ishbaashi T., Kasahara M.;
 RT Structural and phylogenetic analysis of the MHC class I-like Fc
 RT receptor gene.
 RL J. Immunol. 154:5907-5918(1995).
 DR EMBL, D37913; BAA07139.1; JOINED.
 DR EMBL, D37912; BAA07139.1; JOINED.
 DR EMBL, D37903; BAA07134.1; JOINED.
 DR EMBL, D37902; BAA07134.1; JOINED.
 DR EMBL, D37905; BAA07135.1; JOINED.
 DR EMBL, D37904; BAA07135.1; JOINED.
 DR EMBL, D37907; BAA07136.1; JOINED.
 DR EMBL, D37906; BAA07136.1; JOINED.
 DR EMBL, D37911; BAA07138.1; JOINED.
 DR EMBL, D37910; BAA07138.1; JOINED.
 DR HSPB, P13599; 3FRU.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF00129; MHC_I.
 DR PRINTS; PR01638; MHCCLASSI.
 DR Prodom; PD000050; MHC_I.1.
 KW Receptor.
 KW NON_TER
 PT NON_TER
 FT 177 177
 SQ SEQUENCE 177 AA; 20385 MW; 228E2AF08B8D62252 CRC64;

Query Match 74.1%; Score 43; DB 11; Length 177;
 Best Local Similarity 77.8%; Pred. No. 6.5;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 TGMGPDPY 9
 Db 25 TGMGPDPY 33

RESULT 3

ID Q30544 PRELIMINARY; PRT; 286 AA.
 AC Q30544;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE ACCE.
 GN ACCE.
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.
 NCBI_TaxID=176299;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C58;
 RX MEDLINE=95113783; PubMed=7814335;
 RA Hwang I., Cook D.M., Farrand S.K.;
 RT "A new regulatory element modulates homoserine lactone-mediated
 RT autoinduction of Ti plasmid conjugal transfer."
 RT J. Bacteriol. 177:449-458(1995).

[2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=C58;
 RC MEDLINE=96312367; PubMed=8763953;
 RX MEDLINE=96312367; PubMed=8763953;
 RA Farrand S.K., Hwang I., Cook D.M.;
 RT "The tra region of the nopaline-type Ti plasmid is a chimera with
 RT elements related to the transfer systems of RSP1010, RP4, and P.";
 RT J. Bacteriol. 178:4233-4247(1996).
 RN (3)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C58;
 RX MEDLINE=96053873; PubMed=9393724;
 RA Kim H., Farrand S.K.;
 RT "Characterization of the acc operon from the nopaline-type Ti plasmid
 RT pTiC58, which encodes utilization of agrocinopines A and B and
 RT susceptibility to agrocin 84.";
 RT J. Bacteriol. 179:7559-7572(1997).
 RN (4)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C58;
 RX Kim H., Farrand S.K.;
 RA Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN (5)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C58;
 RX Piper K.R., Beck von Bodman S., Cook D.M., Hwang I., Kim H.,
 RA Farrand S.K.;
 RA Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 RN (6)
 RP EMBL, AF010180; AAC17201.1;
 DR InterPro; IPR000515; BPD_transp.
 DR Pfam; PF00528; BPD_transp.
 DR PROSITE; PS00402; BPD_TRANSP_INN_MEMBER; UNKNOWN_1.
 KW Plasmid.
 SQ SEQUENCE 286 AA; 31025 MW; 1DBA970800F08C70 CRC64;

Query Match 70.7%; Score 41; DB 2; Length 286;
 Best Local Similarity 85.7%; Pred. No. 24;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 3 WLAGPDPY 9
 Db 43 WLAGPDPY 49

RESULT 4

ID Q9R6D6 PRELIMINARY; PRT; 286 AA.
 AC Q9R6D6;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE TIORF124 protein.
 GN TIORF124.
 OS Agrobacterium tumefaciens.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.
 NCBI_TaxID=358;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF301001;
 RX MEDLINE=201844752; PubMed=10721727;
 RA Suzuki K., Hattori Y., Uraji M., Ohta N., Iwata K., Murata K.,
 RA Kato A., Yoshida K.;
 RT "Complete nucleotide sequence of a plant tumor-inducing Ti plasmid."
 RT Gene. 242:331-336(2000).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF301001;
 RX MEDLINE=98193120; PubMed=9524202;
 RA Suzuki K., Ohta N., Hattori Y., Uraji M., Kato A., Yoshida K.;
 RT "Novel structural difference between nopaline- and octopine-type trbJ
 RT gene: construction of genetic and physical map and sequencing of

Run on: April 16, 2003, 16:56:17 ; Search time 7.13684 Seconds
(without alignments)
168.037 Million cell updates/second

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

searched: 908470 seqs, 133250620 residues
To number of hits satisfying chosen parameters: 908470

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing:	Minimum Match	0%
	Maximum Match	100%
	Listing first	45 summaries

Database

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13	/SID2/gcgdata/genseq/genseqp-emb1/AA1992.DAT *
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15	/SID2/gcgdata/genseq/genseqp-emb1/AA1994.DAT *
16	/SID2/gcgdata/genseq/genseqp-emb1/AA1995.DAT *
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18	/SID2/gcgdata/genseq/genseqp-emb1/AA1997.DAT *
19	/SID2/gcgdata/genseq/genseqp-emb1/AA1998.DAT *
20	/SID2/gcgdata/genseq/genseqp-emb1/AA1999.DAT *
21	/SID2/gcgdata/genseq/genseqp-emb1/AA2000.DAT *
22	/SID2/gcgdata/genseq/genseqp-emb1/AA2001.DAT *
23	/SID2/gcgdata/genseq/genseqp-emb1/AA2002.DAT *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
	1	58	100.0	9	22	AAB67492	Human heavy chain
	2	58	100.0	9	22	AAB67497	Human heavy chain
	3	58	100.0	118	22	AAB67508	light chain variab
	4	58	100.0	118	22	AAB67509	light chain variab
	5	58	100.0	118	22	AAB67513	Heavy Chain variab
	6	58	100.0	118	22	AAB67515	Heavy Chain variab
	7	46	79.3	599	22	AAV72375	Ampliphilic recomb
	8	40	69.0	163	21	AAV93725	The heavy chain of
	9	39.5	68.1	41	22	ABR86612	Peptide #1263 enco
	10	39.5	68.1	41	22	ABR37955	Peptide #1101 enco

11	39.5	68.1	41	22	ABM19235	Protein #1237 encod
12	39.5	68.1	41	22	AAH64551	Human brain expres
13	39.5	68.1	41	22	AAH66968	Human bone marrow
14	39.5	68.1	41	22	AAH41488	Peptide #1162 encod
15	39.5	68.1	41	22	AAH47255	Peptide #1192 encod
16	39.5	68.1	41	22	AAH02553	Peptide #1135 encod
17	39.5	68.1	41	22	ABG36625	Human peptide encod
18	39	67.2	67	20	AAH11877	Human 5' EST secret
19	39	67.2	67	22	ABH31004	Peptide #3655 encod
20	39	67.2	67	22	ABH21572	Protein #3571 encod
21	39	67.2	67	22	AAH17193	Peptide #3627 encod
22	39	67.2	79	20	AAH11647	Human 5' EST secret
23	39	67.2	100	23	ABH78659	Human scml2 transpo
24	39	67.2	354	22	AAH82604	Cattle IgG transpo
25	39	67.2	354	22	AAH82606	Sheep IgG transpo
26	39	67.2	383	21	AAH38442	Fragment of human
27	39	67.2	577	18	AAH37338	Human sex comb on
28	39	67.2	577	18	AAH37338	Human sex comb on
29	39	67.2	577	20	AAH18284	Human Scm protein
30	39	67.2	591	18	AAH37399	Human Scm protein
31	39	67.2	591	18	AAH37395	Human sex comb on
32	39	67.2	591	20	AAH18289	Human sex comb on
33	39	67.2	620	18	AAH37397	Human Scm protein
34	39	67.2	620	18	AAH37393	Human sex comb on
35	39	67.2	620	20	AAH18287	Human sex comb on
36	39	67.2	623	22	ABG03903	Human Scm protein
37	39	67.2	648	22	AAH94447	Novel1 human diag
38	39	67.2	664	18	AAH37400	Human protein sequ
39	39	67.2	664	18	AAH37396	Mouse sex comb on
40	39	67.2	664	20	AAH18290	Mouse sex comb on
41	39	67.2	730	22	ABG28448	Mouse Scm protein
42	39	67.2	827	22	AAH07864	Novel human diag
43	39	67.2	877	22	ABH64464	Polypeptide sequen
44	38	65.5	54	22	AAH53535	Drosophila melanog
45	38	65.5	21	21	AAH14306	Propionibacterium
						Human secreted pro

ALIGNMENTS

RESULT 1
AAB67492

AC AAB67492;

DT 29-MAY-2001 (first entry)

Human heavy chain complementarity determining region 3 (CDR3) .

Complementarity determining region; CDR; Immune response; antibody; cytotoxic T lymphocyte associated antigen 4; CD4; CD4⁺

KW autoimmune disease; infectious disease; inflammation; allergy;
KW rheumatoid arthritis; myasthenia gravis; typhus erythematosa;

multiplicities; insulin-dependent diabetes mellitus; inflammation;
transplant rejection; graft versus host disease.

OS Homo sapiens

PN WO200114424-A2

PD 01-MAR-2001.
xy

24-AUG-2000; 2000WO-US23356.

PK 24-AUG-1999; 99US
XX

[illegible]

XX

10

PD 01-MAR-2001.
 XX 24-AUG-2000; 2000WO-US23356.
 XX 24-AUG-1999; 99US-0150452.
 XX (MEDA-) MEDAREX INC.
 XX Korman AJ, Halk EL, Lonberg N;
 XX WPI; 2001-202933/20.
 XX
 PT Novel human sequence antibody that binds to human cytotoxic T
 PT lymphocyte associated antigen-4, useful for inducing, augmenting or
 PT prolonging immune response to antigen or for suppressing immune
 PT response in patient
 XX
 PS Claim 25; Fig 8; 127pp; English.
 XX
 CC The present sequence represents the heavy chain variable region of
 CC human antibody 10D1. This antibody specifically binds to human
 CC cytotoxic T lymphocyte associated antigen-4 (CTLA-4). Such antibodies
 CC are used in methods for inducing, augmenting or prolonging an immune
 CC response to an antigen in a patient, where the antibodies block
 CC binding of human CTLA-4 to human B7 ligands. The antibodies are
 CC also useful for treating autoimmune disease in a subject caused or
 CC exacerbated by increased activity of T cells and for treating prostate
 CC cancer, melanoma or epithelial cancer. A polyvalent or polyclonal
 CC antibody preparation comprising two antibodies of the invention are
 CC useful for suppressing an immune response in a patient. They are used for
 CC treating cancer, infectious diseases and promoting beneficial autoimmune
 CC reactions for the treatment of diseases with inflammatory or allergic
 CC components. The polyvalent or polyclonal preparations are useful for
 CC treating autoimmune diseases such as rheumatoid arthritis, myasthenia
 CC gravis and lupus erythematosus, multiple sclerosis, insulin-dependent
 CC diabetes mellitus, transplant rejection, and inflammation, graft versus
 CC host disease.
 XX
 SQ Sequence 118 AA;
 XX
 QY Query Match 100.0%; Score 58; DB 22; Length 118;
 DB Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGMGPFDPY 9
 DB 99 TGMGPFDPY 107
 REPEAT 6
 AAB67514
 ID AAB67514 standard; peptide; 118 AA.
 XX
 AC AAB67514;
 XX
 DT 29-MAY-2001 (first entry)
 XX
 DE Heavy chain variable region of anti-CTLA-4 antibody 10D1.
 XX
 KW Complementarity determining region; CDR; immune response; antibody;
 KW cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;
 KW autoimmune disease; infectious disease; inflammation; allergy;
 KW rheumatoid arthritis; myasthenia gravis; lupus erythematosus;
 KW multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;
 KW transplant rejection; graft versus host disease.
 XX
 OS Homo sapiens.
 XX
 PH Key
 FT Location/Qualifiers
 FT 31..35
 FT /note= "CDR1"
 FT 50..66
 FT /note= "CDR2"
 FT Region
 FT

FT Region 99..107
 FT /note= "CDR3"
 XX
 PN WO200114424-A2.
 XX
 PD 01-MAR-2001.
 XX
 PF 24-AUG-2000; 2000WO-US23356.
 XX
 PR 24-AUG-1999; 99US-0150452.
 XX
 XX (MEDA-) MEDAREX INC.
 XX Korman AJ, Halk EL, Lonberg N;
 XX WPI; 2001-202933/20.
 XX
 DR Novel human sequence antibody that binds to human cytotoxic T
 DR lymphocyte associated antigen-4, useful for inducing, augmenting or
 DR prolonging immune response to antigen or for suppressing immune
 DR response in patient
 XX
 PS Claim 26; Fig 8; 127pp; English.
 XX
 CC The present sequence represents the heavy chain variable region of
 CC human antibody 10D1. This antibody specifically binds to human
 CC cytotoxic T lymphocyte associated antigen-4 (CTLA-4). Such antibodies
 CC are used in methods for inducing, augmenting or prolonging an immune
 CC response to an antigen in a patient, where the antibodies block
 CC binding of human CTLA-4 to human B7 ligands. The antibodies are
 CC also useful for treating autoimmune disease in a subject caused or
 CC exacerbated by increased activity of T cells and for treating prostate
 CC cancer, melanoma or epithelial cancer. A polyvalent or polyclonal
 CC antibody preparation comprising two antibodies of the invention are
 CC useful for suppressing an immune response in a patient. They are used for
 CC treating cancer, infectious diseases and promoting beneficial autoimmune
 CC reactions for the treatment of diseases with inflammatory or allergic
 CC components. The polyvalent or polyclonal preparations are useful for
 CC treating autoimmune diseases such as rheumatoid arthritis, myasthenia
 CC gravis and lupus erythematosus, multiple sclerosis, insulin-dependent
 CC diabetes mellitus, transplant rejection, and inflammation, graft versus
 CC host disease.
 XX
 SQ Sequence 118 AA;
 XX
 QY Query Match 100.0%; Score 58; DB 22; Length 118;
 DB Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGMGPFDPY 9
 DB 99 TGMGPFDPY 107
 RESULT 7
 AAY72375
 ID AAY72375 standard; Protein; 599 AA.
 XX
 AC AAY72375;
 XX
 DT 24-APR-2001 (first entry)
 XX
 DE Amphiphilic recombinant collagen-like polymer, NIN2P4.
 XX
 KW Recombinant protein; collagen-like polymer; gelatin-like polymer; NIN2P4;
 KW stabiliser; oil-in-water emulsion; foodstuff; pharmaceutical product;
 KW cosmetic product; photography.
 XX
 OS Synthetic.
 XX
 XX EP1063565-A1.
 XX 27-DEC-2000.
 PD

XX 23-JUN-2000; 2000EP-0202206.
 PF 24-JUN-1999; 99EP-0202047.
 PR (FUUF) FUUF PHOTO FILM BV.
 PA
 XX
 PI Olive JH, Bouwstra JB, De Wolf FA, Werten MWT, Wisselink HM;
 PI Wind RD, Van Den Bosch TJ, Toda Y;
 XX WPI; 2001-125578/14.
 DR
 XX Oil-in-water emulsions for preparing foodstuffs, pharmaceutical product
 PT or cosmetic product, comprises recombinant collagen-like polymer as
 PS stabilizer
 CC Example 6; Page 24-26; 31pp; English.
 XX
 CC The present sequence is a synthetic amphiphilic recombinant collagen-
 CC like (or gelatin-like) polymer, N1N2P4 which contains two different
 CC in-polar modules (N1) and four polar modules (P4). The N2 module
 CC is similar to the N1 module, but differs mainly in the presence of
 CC a cluster of methionine and charged residues at its C-terminal side.
 CC This polymer exhibits an amphiphilic structure and is used as a
 CC stabiliser for oil-in-water emulsions. The oil-in-water emulsion is
 CC used for producing foodstuffs, pharmaceutical products or cosmetic
 CC products by combining with nutritionally, pharmaceutically, and
 CC cosmetically suitable ingredients. It is also useful in photography.
 CC
 SO Sequence 599 AA;

Query Match 79.3%; Score 46; DB 22; Length 599;
 Best Local Similarity 87.5%; Pred. No. 9.5;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 GMLGPPDY 9
 DB 142 GMLGPPGY 149

RESULT 8
 ID AAY93725 standard; Protein; 163 AA.
 AC AAY93725;
 XX
 DT 03-OCT-2000 (first entry)
 XX
 DE ie heavy chain of immunoglobulin clone 12.9.1.1.

XX Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
 KM hyperimmune disorder; autoimmune disease; diabetes; graft rejection;
 KW proliferative disorder; cancer; immunodeficient disorder.
 XX Homo sapiens.
 OS
 PN WO200037504-A2.
 XX
 PD 29-JUN-2000.
 XX
 PF 23-DEC-1999; 99MO-US30895.
 XX
 PR 23-DEC-1998; 98US-0113647.

XX (PFI2) PRIZER INC.
 PA (ABGE-) ABGENIX INC.
 XX
 PI Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;
 PI Corvaian JR;
 XX WPI; 2000-442647/38.
 DR N-PSDB; AAA46888.
 XX

PT Novel antibodies capable of binding cytotoxic T-lymphocyte antigen
 PT (CTLA)-4 containing specified heavy and light chain sequences, useful
 PT for treating, e.g. immune disorders
 XX
 XX Claim 2; Fig 1W; 157pp; English.
 PS
 CC

CC The present sequence represents a heavy chain of an antibody of the
 CC invention. The antibody is directed cytotoxic T-lymphocyte antigen
 CC (CTLA)-4. Antibodies of the invention are composed of a heavy chain
 CC variable region, comprising a modified contiguous sequence from a
 CC FRI-FR3 sequence encoded by a human VH3-33 family gene. The
 CC modifications are contained in CDR1, CDR2 and/or framework regions.
 CC The antibodies may be used to inhibit CTLA-4 and down-regulate the
 CC immune system to treat hyperimmunity disorders (e.g. autoimmune
 CC disease, diabetes and graft rejection) and proliferative disorders
 CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate
 CC immune system to up-regulate immunodeficient disorders.
 CC
 SO Sequence 163 AA;

Query Match 69.0%; Score 40; DB 21; Length 163;
 Best Local Similarity 66.7%; Pred. No. 26;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 TGMVGPPDY 9
 DB 91 TGMVGPPDF 99

RESULT 9
 ID ABB28612 standard; Peptide; 41 AA.
 AC ABB28612;
 XX
 DT 01-FEB-2002 (first entry)
 XX
 DE Peptide #1263 encoded by breast cell single exon nucleic acid probe.
 XX
 KM Human; microarray; single exon probe; gene expression; breast;
 KM disease; cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200157271-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US00662.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX

PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-496933/54.
 XX

PT New spatially-addressable set of single exon nucleic acid probes,
 PT useful for measuring gene expression in sample derived from human
 PT breast, comprises number of single exon nucleic acid probes
 XX
 PS Claim 27; SEQ ID NO 11580; 327pp + sequence listing; English.
 XX

CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human breast and BT 474 cells. The method involves contacting

CC the probes with a collection of detectably labelled nucleic acids
 CC derived from mRNA of human breast, and then measuring the label
 CC bound to each probe of the microarray. The probes are useful for
 CC verifying the expression of regions of genomic DNA predicted to
 CC encode proteins. They are useful for gene discovery, and for
 CC determining predisposition and/or prognosing breast disease. Gene
 CC expression analysis is useful for assessing the toxicity of chemical
 CC agents on cells. The microarray of this invention presents a far greater
 CC diversity of probes for measuring gene expression, with far less bias
 CC than expressed sequence tag microarrays. The method is suitable for
 CC rapid production of functional information from genomic sequence. The
 CC present sequence is a peptide encoded by a single exon nucleic acid
 CC probe of the invention.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 SQ Sequence 41 AA;
 Y Match 68.1%; Score 39.5; DB 22; Length 41;
 Local Similarity 66.7%; Pred. No. 7.5;
 Matches 8; Conservative 0; Mismatches 1; Indels 3; Gaps 1;
 QY 1 TGMIGP---FDY 9
 Db 1 TGMIGPVSIFGY 12
 RESULT 10
 ABB33795
 ID ABB33795 standard; Peptide; 41 AA.
 AC ABB33795;
 XX
 DT 04-FEB-2002 (first entry)
 XX
 DE Peptide #1301 encoded by human foetal liver single exon probe.
 XX
 KM Human; foetal liver; gene expression; single exon nucleic acid probe.
 XX
 OS Homo sapiens.
 XX
 PN WO200157277-A2.
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US00669.
 XX
 PR 4-FEB-2000; 2000US-0180312.
 XX
 PR 26-MAY-2000; 2000US-0207456.
 XX
 PR 30-JUN-2000; 2000US-0608408.
 XX
 PR 03-AUG-2000; 2000US-0632366.
 XX
 PR 21-SEP-2000; 2000US-0234687.
 XX
 PR 27-SEP-2000; 2000US-0236359.
 XX
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-483447/52.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for
 XX
 PT analyzing gene expression in human foetal liver -
 XX
 XX Claim 27; SEQ ID NO 26430; 639pp + sequence listing; English.
 CC The invention relates to a single exon nucleic acid probe for
 CC measuring human gene expression in a sample derived from human foetal
 CC liver. The single exon nucleic acid probes may be used for predicting,
 CC measuring and displaying gene expression in samples derived from human
 CC foetal liver. The present sequence is a peptide encoded by a single exon
 CC nucleic acid probe of the invention.

CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 SQ Sequence 41 AA;
 Query Match 68.1%; Score 39.5; DB 22; Length 41;
 Best Local Similarity 66.7%; Pred. No. 7.5;
 Matches 8; Conservative 0; Mismatches 1; Indels 3; Gaps 1;
 QY 1 TGMIGP---FDY 9
 Db 1 TGMIGPVSIFGY 12
 RESULT 11
 ABB19238
 ID ABB19238 standard; Protein; 41 AA.
 AC ABB19238;
 XX
 DT 23-JAN-2002 (first entry)
 XX
 DE Protein #1237 encoded by probe for measuring heart cell gene expression.
 XX
 KM Human; gene expression; heart; microarray; vascular system;
 KM cardiovascular disease; hypertension; cardiac arrhythmia;
 KM congenital heart disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200157274-A2.
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US00666.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 XX
 PR 26-MAY-2000; 2000US-0207456.
 XX
 PR 30-JUN-2000; 2000US-0608408.
 XX
 PR 03-AUG-2000; 2000US-0632366.
 XX
 PR 21-SEP-2000; 2000US-0234687.
 XX
 PR 27-SEP-2000; 2000US-0236359.
 XX
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-488899/53.
 XX
 PT Single exon nucleic acid probes for analyzing gene expression in human
 XX
 PT hearts -
 XX
 XX Claim 15; SEQ ID NO 21008; 530pp; English.
 CC The present invention relates to single exon nucleic acid probes for
 CC measuring human gene expression in a sample derived from human heart (see
 CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
 CC probe. The probes may be used for predicting, measuring and displaying
 CC gene expression in samples derived from the human heart via microarrays.
 CC By measuring gene expression, the probes are useful for predicting
 CC diagnosing, grading, staging, monitoring and prognosing diseases of the
 CC human heart and vascular system e.g. cardiovascular disease,
 CC hypertension, cardiac arrhythmias and congenital heart disease.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 SQ Sequence 41 AA;
 Query Match 68.1%; Score 39.5; DB 22; Length 41;
 Best Local Similarity 66.7%; Pred. No. 7.5;

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 17:21:54 (Search time 2.65263 Seconds
(without alignments)
256.547 Million cell updates/sec

Title: US-09-644-668a-37

Perfect score: 58

Sequence: 1 TGMICPPDY 9

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 288829 seqs, 75613885 residues

To: Number of hits satisfying chosen parameters: 288829

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	42	72.4	408 9 US-10-140-372-3	Sequence 3, Appl1
2	39.5	68.1	41 10 US-09-864-761-34536	Sequence 34536, A
3	39	67.2	67 10 US-09-864-761-36870	Sequence 36870, A
4	39	67.2	100 10 US-09-872-523-15	Sequence 15, Appl1
5	39	67.2	383 9 US-10-050-704-239	Sequence 239, Appl1
6	39	67.2	827 10 US-09-801-574-12	Sequence 14, Appl1
7	38	65.5	110 10 US-09-740-668A-14	Sequence 70, Appl1
8	38	65.5	110 10 US-09-915-582-70	Sequence 10, Appl1
9	37	63.8	400 10 US-09-815-242-10380	Sequence 10380, A
10	37	63.8	401 10 US-09-815-242-11155	Sequence 11155, A
11	37	63.8	419 10 US-09-815-242-11798	Sequence 11798, A
12	35.5	61.2	436 9 US-09-738-626-3877	Sequence 3877, Ap
13	35	60.3	15 9 US-09-880-748-2958	Sequence 2958, Ap
14	35	60.3	117 10 US-09-861-451A-70	Sequence 70, Appl1
15	35	60.3	154 10 US-09-925-301-1526	Sequence 1526, Ap
16	35	60.3	252 9 US-09-880-748-1201	Sequence 1201, Ap
17	35	60.3	252 9 US-09-880-748-1519	Sequence 1519, Ap
18	35	60.3	257 9 US-09-738-626-6656	Sequence 6656, Ap
19	35	60.3	431 10 US-09-815-242-11033	Sequence 11033, A

20	35	60.3	530 9 US-09-738-626-4188	Sequence 4188, Ap
21	35	60.3	1198 9 US-09-975-719-405	Sequence 405, Ap
22	34	58.6	68 9 US-09-796-692-1775	Sequence 1775, Ap
23	34	58.6	77 9 US-09-796-692-2255	Sequence 2255, Ap
24	34	58.6	77 9 US-09-796-692-2265	Sequence 2265, Ap
25	34	58.6	92 10 US-09-764-877-1874	Sequence 1874, Ap
26	34	58.6	141 10 US-09-073-009-15	Sequence 15, Appl1
27	34	58.6	141 10 US-09-023-588-15	Sequence 15, Appl1
28	34	58.6	141 10 US-09-793-306-15	Sequence 15, Appl1
29	34	58.6	151 9 US-10-102-806-435	Sequence 435, Appl1
30	34	58.6	307 10 US-09-036-613-7	Sequence 7, Appl1
31	34	58.6	381 9 US-09-738-626-3549	Sequence 3549, Ap
32	34	58.6	400 10 US-09-073-009-126	Sequence 126, Ap
33	34	58.6	400 10 US-09-793-306-126	Sequence 126, Ap
34	34	58.6	408 9 US-09-813-398-20	Sequence 20, Appl1
35	34	58.6	408 9 US-09-813-398-22	Sequence 22, Appl1
36	34	58.6	412 9 US-09-978-295A-157	Sequence 157, Ap
37	34	58.6	412 9 US-09-978-697-157	Sequence 157, Ap
38	34	58.6	412 9 US-09-978-192A-157	Sequence 157, Ap
39	34	58.6	412 9 US-09-999-832A-157	Sequence 157, Ap
40	34	58.6	412 9 US-10-001-054-8	Sequence 8, Appl1
41	34	58.6	412 9 US-09-978-189-157	Sequence 157, Ap
42	34	58.6	412 9 US-09-978-608A-157	Sequence 157, Ap
43	34	58.6	412 9 US-09-978-191A-157	Sequence 157, Ap
44	34	58.6	412 9 US-09-978-403A-157	Sequence 157, Ap
45	34	58.6	412 9 US-09-978-564A-157	Sequence 157, Ap

ALIGNMENTS

RESULT 1
US-10-140-372-3
Sequence 3, Application US/10140372
Publication No. US20030021789A1
GENERAL INFORMATION:
APPLICANT: XU, YI
TITLE OF INVENTION: SURFACE PROTEINS FROM GRAM-POSITIVE BACTERIA
FILE REFERENCE: P07196US01/BAS
CURRENT FILING DATE: 2002-05-08
PRIOR APPLICATION NUMBER: US 60/289,132
PRIOR FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 408
TYPE: PRT
ORGANISM: Streptococcus mutans
US-10-140-372-3

Query Match 72.4%; Score 42; DB 9; Length 408;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGMICPPDY 9
DB 239 SAWINPFDY 247

RESULT 2
US-09-864-761-34536
Sequence 34536, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Penn, Sharon G.
APPLICANT: Hanrel, David R.
APPLICANT: Hanrel, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 34536
LENGTH: 41
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC005519.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.98
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.99
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.93
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
OTHER INFORMATION: EST HUMAN HIT: A0137038.1, EVALUOR 1.00e-17
OTHER INFORMATION: SWISSPROT HIT: Q14678, EVALUOR 1.00e-18
US-09-864-761-34536
Query Match 68.1%; Score 39.5; DB 10; Length 41;
Best Local Similarity 66.7%; Pred. No. 6.9;
Matches 8; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

RESULT 3
US-09-864-761-36870
Sequence 36870, Application US/09864761
Patent No. US20020048763A1

GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmca-X-1
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 36870
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL110502.1
OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 0.93
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.1
OTHER INFORMATION: SWISSPROT HIT: Q01441, EVALUOR 3.00e+00
OTHER INFORMATION: EST_HUMAN HIT: BE257700.1, EVALUOR 4.00e-37
US-09-864-761-36870
Query Match 67.2%; Score 39; DB 10; Length 67;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 4
US-09-872-523-15
Sequence 15, Application US/09872523

GenCore version 5.1.4 p5.4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 17:15:40 ; Search time 2.30526 Seconds
(without alignments)
114.870 Million cell updates/sec

Title: US-09-644-668a-37

Perfect score: 58

Sequence: 1 TGMGPFDPY 9

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

To: number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents, AA:*
1: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
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5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfillseq.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	67.2	577	2	US-08-852-153-4
2	39	67.2	591	2	US-08-852-153-6
3	39	67.2	620	2	US-08-852-153-2
4	39	67.2	664	2	US-08-852-153-8
5	36	62.1	12	2	US-08-406-330-33
6	36	62.1	12	2	US-08-556-597-33
7	35	60.3	121	1	US-08-339-582-2
8	35	60.3	136	4	US-08-559-451-5
9	35	60.3	366	1	US-08-004-492-8
10	35	60.3	432	5	PCT-US93-04910-13
11	35	60.3	433	1	US-07-672-483-4
12	35	60.3	433	4	US-08-259-451-3
13	35	60.3	1198	4	US-09-199-637A-405
14	34	58.6	27	1	US-08-383-753-20
15	34	58.6	27	2	US-08-586-772-20
16	34	58.6	27	2	US-08-959-512-20
17	34	58.6	27	4	US-09-512-983-20
18	34	58.6	262	4	US-09-372-422A-32
19	34	58.6	296	2	US-08-100-637-4
20	34	58.6	307	1	US-07-982-112-2
21	34	58.6	390	4	US-09-134-001C-3112
22	34	58.6	616	2	US-09-001-826-5
23	34	58.6	621	4	US-08-604-789B-4
24	34	58.6	621	4	US-09-312-721A-4
25	34	58.6	621	4	US-08-469-260A-387
26	33	56.9	119	1	US-08-478-039-65
27	33	56.9	119	1	US-08-476-349A-65

28	33	56.9	126	4	US-09-240-274-10	Sequence 10, Appl
29	33	56.9	126	4	US-09-240-274-144	Sequence 144, Appl
30	33	56.9	126	4	US-09-240-274-150	Sequence 150, Appl
31	33	56.9	127	4	US-09-240-274-11	Sequence 11, Appl
32	33	56.9	127	4	US-08-846-762-15	Sequence 15, Appl
33	33	56.9	413	2	US-08-846-762-88	Sequence 88, Appl
34	33	56.9	491	2	US-09-001-826-23	Sequence 23, Appl
35	33	56.9	577	4	US-09-486-382B-2	Sequence 2, Appl
36	33	56.9	577	4	US-09-486-382B-13	Sequence 13, Appl
37	33	56.9	593	5	PCT-US93-07923-11	Sequence 11, Appl
38	33	56.9	595	3	US-08-604-789B-3	Sequence 3, Appl
39	33	56.9	595	4	US-09-312-721A-3	Sequence 3, Appl
40	33	56.9	604	3	US-08-604-789B-2	Sequence 2, Appl
41	33	56.9	604	3	US-08-604-789B-16	Sequence 16, Appl
42	33	56.9	604	4	US-09-312-721A-2	Sequence 2, Appl
43	33	56.9	604	4	US-09-312-721A-16	Sequence 16, Appl
44	33	56.9	606	4	US-09-486-382B-11	Sequence 11, Appl
45	33	56.9	755	5	PCT-US93-07923-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-852-153-4
Sequence 4, Application US/08852153
Patent No. 5914266
GENERAL INFORMATION:
APPLICANT: Randazzo, Filippo
TITLE OF INVENTION: Mammalian Sex Comb on Midleg Acts as a Tumor Suppressor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESS: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
COUNTRY: U.S.A.
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,153
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Guth, Joseph H.
REGISTRATION NUMBER: 31,261
REFERENCE/DOCKET NUMBER: 1224.006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-3888
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 577 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-852-153-4
Query Match 67.2%; Score 39; DB 2; Length 577;
Best Local Similarity 75.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
CY 2 TGMGPFDPY 9
DB 142 GWRGARDY 149
RESULT 2

US-08-852-153-6
Sequence 6, Application US/08852153
Patent No. 5914266
GENERAL INFORMATION:
APPLICANT: Randazzo, Filippo
TITLE OF INVENTION: Mammalian Sex Comb on Midleg Acts as a Tumor Suppressor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
COUNTRY: U.S.A.
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
CLASSIFICATION: 435
FILING DATE:
APPLICATION NUMBER: US/08/852,153

ATTORNEY/AGENT INFORMATION:
NAME: Gutth, Joseph H.
REGISTRATION NUMBER: 31,261
REFERENCE/DOCKET NUMBER: 1224.006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-3888
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 591 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-852-153-6

Query Match
Best Local Similarity 67.2%; Score 39; DB 2; Length 591;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GMLGPFY 9
DB 156 GMRGAFDY 163

RE 3
US-08-852-153-2
Sequence 2, Application US/08852153
Patent No. 5914266
GENERAL INFORMATION:
APPLICANT: Randazzo, Filippo
TITLE OF INVENTION: Mammalian Sex Comb on Midleg Acts as a Tumor Suppressor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
COUNTRY: U.S.A.
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
CLASSIFICATION: 435
FILING DATE:
APPLICATION NUMBER: US/08/852,153

NAME: Gutth, Joseph H.
REGISTRATION NUMBER: 31,261
REFERENCE/DOCKET NUMBER: 1224.006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-3888
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-852-153-2

Query Match
Best Local Similarity 67.2%; Score 39; DB 2; Length 620;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GMLGPFY 9
DB 185 GMRGAFDY 192

RESULT 4
US-08-852-153-8
Sequence 8, Application US/08852153
Patent No. 5914266
GENERAL INFORMATION:
APPLICANT: Randazzo, Filippo
TITLE OF INVENTION: Mammalian Sex Comb on Midleg Acts as a Tumor Suppressor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
COUNTRY: U.S.A.
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
CLASSIFICATION: 435
FILING DATE:
APPLICATION NUMBER: US/08/852,153

US-08-852-153-8
Sequence 8, Application US/08852153
Patent No. 5914266
GENERAL INFORMATION:
APPLICANT: Randazzo, Filippo
TITLE OF INVENTION: Mammalian Sex Comb on Midleg Acts as a Tumor Suppressor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
COUNTRY: U.S.A.
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
CLASSIFICATION: 435
FILING DATE:
APPLICATION NUMBER: US/08/852,153

Query Match
Best Local Similarity 67.2%; Score 39; DB 2; Length 664;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GMLGPFY 9
DB 203 GMRGAFDY 210